STIC-Biotech/ChemLib

154049

From:

Swope, Sheridan

Sent:

Thursday, June 09, 2005 6:04 PM

To:

STIC-Biotech/ChemLib

Subject:

10023515

For 10023515, pls search and interference search:

SID 1 against the NT and AA data bases.

SID 2 against the NT and AA data bases.

SID 3 against the NT and AA data bases.

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E02C70 Remsen Bld (Mailbox)

TOPY

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

Type of Search

NA#:	AA#:
Interference:	SPDI:
S/L:	Oligomer:
Encode/Tran	sl:
Structure#:_	Text:
Inventor:	Litigation:

Vendors and cost where applicable STN:_______
DIALOG:______

QUESTEL/ORBIT:_____ LEXIS/NEXIS:_____ SEQUENCE SYSTEM:____

WWW/Internet:_____ Other(Specify):_____

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Q8NBCB
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Q6AW47
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Q81034
Q95KH3
SASB ANAPL
Q91WG0
Q8BK48
Q3533
Q8BM97
Q6CPDB7
Q6CPS4
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Q6FDB7
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Q6FB107
Q8FB31
EST2_RABIT
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Q61PR9
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SEQUENCE FROM N.A. TISSUE—PCR rescued clones; Director MGC Project; Submitted (APR-2004) to the EMBL/GenBank/DDBJ dat -!- SIMILARITY: Belongs to the type-B carboxylest EMBL; BC069501; AAH69501.1; HSSP; P12337; IKAY. GO; GO:0003824; F:catalytic activity; IEA. InterPro; IPR002018; CarbesteraseB. InterPro; IPR00379; Ser_estrs. Pfam; PF00135; COesterase; 1. PROSITE; PS00122; CARBOXYLESTERASE B 1; 1. PROSITE; PS00941; CARBOXYLESTERASE B 2; 1. Hydrolase. 575 AA; 63926 MW; 6F5B735BDEFC9C09 C	Name=FLJ31547; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebri Eukaryota; Metazoa; Chordata; Craniata; Homin: Homin: Mammalia; Butheria; Primates; Catarrhini; Homin: NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. TISSUE=PCR rescued clones; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/j Strausberg R.L., Feingold E.A., Grouse L.H., Dei Klausner R.D., Collins F.S., Wagner L., Shenmen Altschul S.F., Zeeberg B., Buetow K.H., Schaefe: Hopkins R.F., Jordan H., Moore T., Max S.I., Wal Diatchenko L., Marusina K., Parmer A.A., Rubin (Stapleton M.J., Usdin T.B., Toshiyuki S., Carn. Raha S.S., Loquellano N.A., Peters G.J., Abramse Bosak S.A., McEwan P.J., McKernan K.J., Malek J. Richards S., Worley K.C., Hale S., Garcia A.M., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X. Fahey J., Helton E., Ketteman M., Madan A., Rodi Whiting M., Madan A., Young A.C., Shevchako Y. Blakesley R.W., Touchman J.W., Green E.D., Dick Rodriguez A.C., Grimwood J., Schmutz J., Myers i Krzywinski M.I., Skalska U., Smailus D.E., Schmu Jones S.J., Marra M.A.; "Generation and initial analysis of more than 1: and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (201)	NIC
tterase/lipase family.	idae; Homo. lidae; Homo. spans.242603899; ge J.G., c.M., Schuler G.D., c.F., Bhat N.K., g.J., Hsieh F., g.M., Hong L., t.T.L., Scheetz T.E., inci P. Prange C., m. R.D., Mullahy S.J., A., Gunaratne P.H., Gay L.J., Hulyk S.W., gibbs R.A., gibbs R.A., son M.C., Bouffard G.G., son M.C., Suhterfield Y.S., srch A., Schein J.E., sprch A., Schein J.E., s,000 full-length human	Q95n05 canis famil Q6uww8 homo sapien Q726j1 homo sapien Q8tdz9 homo sapien Q8tcd29 homo sapien Q8tcd1 mus musculu Q91w10 mus musculu Q97882 sus scrofa Q6gmj1 brachydanio Q29550 sus scrofa Q46421 macaca fasc P12337 oryctolagus P23953 mus musculu Q35534 mesocricetu P10959 rattus norv

Query Match

Local

Similarity

94.7%;

Length

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RESULT

Q96DN9
ID
Q96DN9
AC
Q9
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Q9
X PubMed=1470203; DOI=10.1038/ng1285;

What T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

What A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

What A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

What A., Hayashi K., Sato H., Nagai K., Kimura Y., Nagahari K.,

What A., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

What A., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

What A., Wasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

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What A., Watanabi T., Watanabi T., Watanabi K., Watanabi K., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

What A., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

What A., Watanabe M., Hiraoka M., Hotuta T., Kusano J.,

What A., Watanabe S., Yosida M., Hotuta T., Kusano J.,

What A., Watanabe S., Yosida M., Hotuta T., Kusano J.,

What A., Watanabe S., Yosida M., Hotuta T., Kusano J.,

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 28, Last annotation updat.)
125-OCT-2004 (TrEMBLrel. 28, Last annotation updat.)
14ypothetical protein FLJ31547,
18me=FLJ31547;
18me=FLJ31547;
19mo sapiens (Human).
18ukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Primates; Catarrhini; Hominid
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Pred. No. 6.2e-214;
3; Mismatches 6;
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Best Local S
Matches 501
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., McKernan K.J., Abrameon R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
Tenenstion and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Tenenstion and initial analysis of more than 15,000 full-length human
LT 11
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RA Musashino K., Yuuki H., Oshima A., Sasaki N., Actsuka S.,
Voshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Sench A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,
RA Cho T., Yamada K., Pujii Y., Ozaki K., Hirao M., Ohmori Y.,
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Nakagawa K.,
RA Nakai K., Yada T., Namura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
T. Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                  GO; GO:0016787; F:hydrolase activity; IEA InterPro; IPR002018; CarbesteraseB. InterPro; IPR002018; Carbesters. Pfam; PF00135; COesterase; 1. PR0017E; PS00122; CARBOXYLESTBRASE B 1; 1. PROSITE; PS00941; CARBOXYLESTBRASE B 2; 1. Hydrolase; Hypothetical protein. SEQUENCE 525 AA; 58200 MW; 7724878B8A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2004) to the EMBL/GenBa-
-- SIMILARITY: Belongs to the type-B
EMBL; AK056109; BAB71094.1; --
EMBL; BC069548; AAH69548.1; --
EMBL; P12337; 1K4Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PCR rescued clones;
Strausberg R.;
Submitted (APR-2004) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                   Similarity
                                                                                   REATSYPNICCLQNSEWLLLIDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF 150
REATSYPNICLONSEWLLLDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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100 MW; 7724878B8A22F215 CRC64;
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Pred. No. 2.2e
0; Mismatches
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the type-B carboxylesterase/lipase
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RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Chiba Y., Ishida S.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Kanehori K., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y.,
RA Cono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Yoshikawa Y., Mateunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshikawa Y., Mateunawa H., Ichihara T., Shiohata N., Sano S.,
RA Noshiya S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagami A., Pujiwara T.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QANBC8 PRELIMINARY;
QANBC8;
QANBC8;
O1-OCT-2002 (TrEMBLrel. 22, Last se
O1-OCT-2003 (TrEMBLrel. 25, Last ar
O1-OCT-2003 (TrEMBLrel. 25, Last ar
Hypothetical protein FL/33678.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLOPFFFFCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
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on update)
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Best Local S
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- SIMILARITY: Belongs to the type-B
EMBL; AK09997; BAC03565.1; -.

HSSP; P12337; 1K4Y.
GO; GO:0016787; F:hydrolase activity;
InterPro; IPR000379; CarbesteraseB.

InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Makagawa K., Mizushima-Sugano J., Satch T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R. Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                 473
                                                                                                             301
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LGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
                                                                                                                                                                                 GFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDL
                                                                                                                                                                                                                                                                                                                                 DVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES
                                                                                                                                                                                                                                                                                                                                                 DVLVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES
                                                                    LKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
                                                                                                                          LGDVFFVVPALITARYHRDAGAPVYFYBFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF
                                                                                                                                                                  GFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDL
                                                                                                                                                                                                                        ALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEFLDLLSQKAFKAIPSIIGVNSHEC
                                                                                                                                                                                                                                      ALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHEC
                                                                                                                                                                                                                                                                           AGAISVSSLILSPMAKGLPHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSE
                                                                                                                                                                                                                                                                                      AGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSE
                                                       LKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
                                                                                                            LGDVFFVVPAL I TARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF
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99.6%;
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Pred. No. 7.8e-179;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7A188F68C10A9080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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RESULT 4
Q6AW47
ID 06AW47;
ID 06AW47;
AC 06AW47;
AC 05AW47;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Carboxylesterase-like urinary excreted protein.
GN Name=cauxin;
OS Canis familiaris (Dog).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI TaxID=9615;
RN [1] -
RP SEQUENCE FROM N.A.
RA Miyazaki M., Yamashita T., Taira H., Suzuki A.;
RT "cauxin family protein.";
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Q6AW46;

Q6AW46;

Q6AW46;

T 25-OCT-2004 (TrEMBLrel. 28, Created)

T 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

T 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

T 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

E Carboxylesterase-like urinary excreted protein.

N Name=cauxin;

Nus musculus (Mouse).

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;

C Mammalia; Butheria; Rodentia; Sciurognathi; Muridae
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Best Local S
Matches 417
                          SEQUENCE
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--- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EMBL; AB186392; BaD35015.1; ---
GO; GO:0003824; F:Cattalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COGSTECTASE; 1.
PROSITE; PS00142; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00142; CARBOXYLESTERASE_B_2; 1.
Hydrolase.
SEQUENCE 575 AA; 63620 MW; 1005C35E82E1183D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      505
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       FROM N.A.
M., Yamashita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 DLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS
                                                                                                                                                                                                                                                                                                                    VLLPFLFSSAP
                                                                                                                                                                                                                                                                                                                                                    LLQPFFFFCAP
                                                                                                                                                                                                                                                                                                                                                                               GLPLWPAYSQSEQYLKLDLNISVGQKLKEQEVEFWSDTLPLIMSMSTAPPGPPVPLLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRPAFVKADHSDEIRFVFGGAFLKGNIVMFEGATEEEKLLSRKMMRYMANFARTGDPNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKPAFYKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWATFARTGNPNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDATSYPKLCLONSVWLLSDQHFLKVHYPNLEVSEDCLYLNIYAPAHANTGSKLPVMVWF
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ilarity 75.7%;
Conservative 6:
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       Taira
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Pred. No. 4e-163;
1; Mismatches 7
                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
     Ξ.,
       Suzuki
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                                                                                                                                                           update)
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                                                                       Euteleostomi;
; Murinae; Mus
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RESULT 6
Q8103
ID Q810
AC Q810.
DT 01-M
DT 01-M
DT 01-O1-M
DT 01-O1-O
DE Carb
GN Name
OC Feli
OC Euka
OC Euka
OC Euka
OC Euka
OC Mamm
OC Mamm
OC NCBI
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                                                                                              Q81034 PRELIMINARY; PKT; CF01034; Q81034; Q810
                          Name=Cauxin;
Name=Cauxin;
Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
 SEQUENCE
                     NCBI_TaxID=9685;
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FROM

N.A.

ation update) protein.

Euteleostomi; Felis.

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Query Match
Best Local Simi
Matches 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cauxin family protein.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; AB186393; BaD35016.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00112; CARBOXYLESTERASE_B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B 2; 1.
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SEQUENCE
    546
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                                                 Similarity 68.9
ILSASKALLSPTFSLILLSLLSPVLLSAA
                                                                                                                    AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLS
                         ILSASDMLHSPLSSLTFLSLLQPFFFFCA
                                                                                                    SGGPVYFYBFQHRPHCFQNSRPAFVKADHTDEIRFVFGGPFLKGDVVMFEBATEBEKLLS
                                                                                                                                                         LALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRD
                                                                                                                                                                                                            KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
                                                                                                                                                                                                                                                                  HRAIMQSGVAIIPSLKSSDNDLKHDLQVVANVCDCNVSDSKALLKCLREKSSLELMSLSQ
                                                                                                                                                                                                                                                                                   HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ
                                                                                                                                                                                                                                                                                                                                      WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                                                                                                                                                                                                                                                                                                                                                         QNQHAPGNWAFWDQLAALLWVRENIKYFGGNPDSVTIFGNSAGAISISSLILSPLSADLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 AA; 64166 MW;
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Pred. No. 3e-1:
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSVTEEPHRYTKLGWVQGKQATVLGRLEPVNVFLGIPFAAP
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                         580
574
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RESULT
Q95KH3
ID Q99
AC Q9
DT 011
DT 011
DT 011
DT 01
DT 01
OC EN
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                                                               Q95KH3; PRELIMINARY;
Q95KH3; O1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia; Butheria; Primates; Catarrhini; Cercopitheci Cercopithecinae; Macaca.

NCBI_TaxID=9541;
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SEQUENCE
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Local Similarity 71.7%;
nes 373; Conservative 6
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                                                                                                                                                                               NDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTI 549
                                                                                                                                                                                                                                                                                                                     LDLLSQKAPKAIPSIIGVNNHECGFLLPMKEAPBILSGSNKSLALHLIQNILHIPPQYLH
                                                                                                                                                                                                                                                                                                                                                                DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REATSYPNICLQNSEWLLLDQHMLKVHYPKFGVSBDCLYLNIYAPAHADTGSKLPVLVWF 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPAADAPVRSTRIGWVRGKQTTVLGSTVPVNMFLGIPYAAPPLGPLRFKQPKPALPGNDF
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                                                                                                                                                                                                                           | DTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNG
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                                                                                                                                                                                                                                                                                                         VALLTOKAFNSVPSIIGVNNHECAFLL-STEFSBILGGSNRSLALYLVHTFLNIPTQYLH
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Pred. No. 6.5e-
60; Mismatches
                                                                  Last sequence up
                                                                                         Created)
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                                                                                                                361
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ches 85;
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                       Cercopithecidae;
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                                                                 update)
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                                   Euteleostomi;
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Q04791;
Q1-FEB-1995
            Hwang C.-S., Kolattukudy P.E.;

"Molecular cloning and sequencing of thioesterase B cDNA and stimulation of expression of the thioesterase B gene associated with hormonal induction of peroxisome proliferation.";

J. Biol. Chem. 268:14278-14284 (1993).

-I- FUNCTION: Fatty acid biosynthesis chain termination and release of the free fatty acid product is achieved by hydrolysis of the thioester by a thioesterase. This thioesterase may be associated with peroxisome proliferation and may play a role in the production of 3-hydroxy fatty acid diester pheromones.

-I- TISSUE SPECIFICITY: Highest levels in uropygial gland, much lower in liver and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                               ANAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Temporal lobe right;
Osada N., Hida M., Kusuda J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO02018; CarbesteraseB.
Pfam; PF00135; COesterase; 1.
Hypothetical protein.
SEQUENCE 361 AA; 41032 MW; AC62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki Y., Sugano S., Hashimoto K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/l
EMBL; AB060873; BAB46884.1; -.
HSSP; P12337; IKAY.
   +
                                                                                                                                                                                     TISSUE=Uropygial gland;
MEDLINE=93300823; PubMed=8314791;
                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-CCT-2004 (Rel. 45, Last amotation update)
Fatty acyl-CoA hydrolase precursor, medium ch
                                                                                                                                                                                                                                               NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                           Anas platyrhynchos (Domestic duck).
                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                           (Thioesterase B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEFWTSTIPLILSASDTLHSPLSFLIFLSLLQPFFFSCVP 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEILSGSNKSLALHLIQNILHIPPQYLHLVANBYFHDKHSLTEIRDSLLDLLGDVFFVVP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                              etazoa; Chordata; Craniata; Vertebrata; Eu
Aves; Neognathae; Anseriformes; Anatidae;
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.4%;
95.0%;
 to the type-B
                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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   carboxylesterase/lipase family
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                                                                                                                                                                                                                                                                                Euteleostomi;
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"HETEROS IPRO02018; CarbesteraseB.

R Interpro; IPR002019; Ser_estrs.

R Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOVE.

Directions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 265; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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 550
                              556
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RRRKHTDL 557
                                                                                                                                            VYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMM
                                                                                                                                                                                                      LHI-----PPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LREATSYPNICLONSEWILLIDOHML-----KVHYPKFGVSEDCLYLNIYAPAHADTGSKL
                              SDMLHSPL
                                                                                KYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSA 555
                                                                                                                    VYFYEFOHRPSSAAGVVPEFV
                                                                                                                                                                                                                                      GVFFFKSPRQLLSEKVINAVPYIIGVNNCEFGWILFRMMKFPEFTEGLEKDVARQVLQST
                                                                                                                                                                                                                                                           GAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP-MKEAPEILSGSNKSLALHLIQNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRDAASYPPMCLQDK---VLGQYLSDAITNRKEKVRLQISEDCLYLNVYTPVSTEEQEKL
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PS00941; CARBOXYLESTERASE B 2; 1.
rotein sequencing; Fatty acid biosynthesis; Hydrolase; Signal.
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Acyl-ester intermediate (By Sil-Charge relay system (By Sil-Charge relay system (By Sil-By Similarity.
N-linked (GlcNAc. . .) (Pol-
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Pred. No. 1.9e-90;
9; Mismatches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iate (By similarity).
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  (By similarity).
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RX MEDLINE-E22744052; PubMed=1285986; DOI=10.1016/S0003-9861(03)00286-8;

RA MEDLINE-22744052; PubMed=1285986; DOI=10.1016/S0003-9861(03)00286-8;

RA Furihata T., Hosokawa M., Nakata F., Satoh T., Chiba K.;

RT Purification, molecular cloning, and functional expression of inducible mouse liver acylcarnitine hydrolase in C57BL/6 mouse, rounded to the carboxylesterase multigene family.";

RT belonging to the carboxylesterase multigene family.";

CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

DR EMBL; BC015290; AAH15290.1; -.

DR EMBL; BC034170; AAH31170.1; -.

DR EMBL; BC034170; AAH34178.1; -.

DR EMBL; BC034170; AAH34178.1; -.

DR EMBL; BC034191; AAH34191.1; -.
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RP SEQUENCE FROM N.A.

RC STRAIN=FUB/N; TISSUE=Colon, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

"Generation and initial analysis of more than 15.000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Submitted
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Q91WG0;
Q91WG0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase 2 (Carboxylesterase ML3 precursor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
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Strausberg R.;
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STRAIN=FVB/N; TISSUE=Kidney;
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUL-2002) to the
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TISSUE=Colon;
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Best Local (
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Q8BK48;
                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RIKEN musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, Clone: 9031415B19 product: similar
to CARBOYLLESTERASE (E 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
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PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

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                          Eukaryota; Metazoa;
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                                                                                                     (9030624L02Rik protein)
Name=9030624L02Rik;
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                          Craniata; Vertebrata; Sciurognathi; Muridae;
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                             Euteleostomi;
; Murinae; Mus
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C STRAIN-C57BL/6J; TISSUE-Ovary and uterus;

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(A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

(A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

(A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

(A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

(A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

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(A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

(A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

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Stlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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MEDLINB-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINB-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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STRAIN=C57BL/6J; TISSUE=Ovary and U
MEDLINE=99279253; PubMed=10349636;
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MEDLINE=20499374; PubMed=11042155; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                             CTRAIN=FVB/N; TISSUE=Colon;
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"High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Ovary The FANTOM Consortium,
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MEDLINE=21085660;
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420:563-573(2002).
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6J; TISSUE=Ovary
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; PubMed=11217851;
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; DOI=10.1038/35055500
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; DOI=10.1016/S0076-6879(99)03004-9;
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on functional annotation
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Best Local :
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PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
SEQUENCE 559 AA.
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MGD; MGI:2443170; 9030624L02Rik.

GO; GO:0005615; C:extracellular space;
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2003) to the EMB-I- SIMILARITY: Belongs to the EMBL; AK077248; BAC36707.1; -- EMBL; BC055062; AAH55062.1; --
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STRAIN=FVB/N; TISSUE=Colon;
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                YWATFARTGNENGNDLSLWEAYNLTEQYLQLDLNMSLGQRLKEERVDEWTSTIP
                                                                 YFYEFQHRPSFFKDFRPPYVKADHGDEIFLVFGYQF--GNIKL--PYTEBEBQLSRRIMK
                                                                                                   M-----LPPECGDLLMEEYMGDTEDPETLQAQFREMKGDFMFVIPALQVAHFQR-SHAPV
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                                                                                                                                                                                                                                                                                                           IHĠĠĀLTVĊMĀŚMYĎĠŚMĹĀĀTĖĎVVVVAIQYRĹĠVĻĠFFSTGDQHĀKĠNWGYLDQVĀĀĹ
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Pred. No. 4.
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carboxylesterase/lipase
VGRALKARRLQFWTKTLP
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P SEQUENCE FROM N.A.

C STRAIN=Syrian golden; TISSUE=Liver;

A Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;

A Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;

L Submitted (MAY-1955) to the EMBL/GenBank/DDBJ databases.

C -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family 150577; BAA23605.1; -.

R EMBL; D50577; BAA23605.1; -.

R HSSP; P12337; 1K4Y.

R GO; GO:0004091; F:carboxylesterase activity; IEA.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0016787; F:hydrolase activity; IEA.

R InterPro; IPR0002018; CarbesteraseB.

InterPro; IPR000379; Ser_estrs.

DR InterPro; IPR000379; Ser_estrs.

DR PROSITE; PS00011; CARBOXYLESTERASE B 1; 1.

DR PROSITE; PS00014; ER TARGET; UNKNOWN_1.
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Best Local Similarity
Matches 262; Conserv
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SIGNAL
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STRAIN-Syrian golden; TISSUE=Liver;

SONE T., Wang C.Y.;

"Microsomal amidases and carboxylesterases.";

(In) Guengerich F.P. (eds.);

COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransfo;

Pergamon, Oxford (1997).
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O35533;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence up
O1-MAR-2004 (TrEMBLrel. 26, Last annotation
Carboxylesterase precursor (EC 3.1.1.1).
Mesocricetus auratus (Golden hamster).
Mesocricetus auratus (Trembler 1.1.1)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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01-MAR-2003
01-MAR-2003
                                                                                                             MEDLINE-2053091; PubMed-i1076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watatahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Miramateu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=CS7BL/6G; TISSUE=Colon;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

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Konno H., Okazaki Y., Muzamatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male colon cDNA, RIKEN full-length enriched
Library, clone:9030624L02 product:similar to CARBOXYLESTERASE (EC
3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE).
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STRAIN-C57BL/6J; TISSUE-Colon;
STRAIN-C57BL/6J; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Hayashizaki Y.; "High-efficiency full-length of Meth. Enzymol. 303:19-44(1999)
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STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
Adachi J., Aizawa K., Akimura
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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409:685-690(2001)
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78; Mismatches 166;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F. Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Rahey J., Helton E., Ketteman M., Madan A., Godrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marram M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 273; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Hypothetical protein.
SEQUENCE 556 AA; 61927 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00122; CARBOXYLESTERASE B 1; 1. 1. PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002018; CarbesteraseB
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                  RTKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPM 358
                                                                                                                                                                                            SSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVNVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHY 118
RGKSEAEILAINKLVQMIPAVVDGEFFPRHPKELLASEDFHPVPSIIGVNNDEFGWTIP-
                                                                                                                                                                                                                                                                 IQYRLGVLGFFSTGDQHARGNWGFLDQVAALRWIQQNIAHFGGKPDRVTIFGESAGGTSV
                                                                                                                                                                                                                                                                                                                    PPVSTSEDCLYLNIYTPAHAHEGSNLPVMVWIHGGGLVAGMASMYDGSLLAAIEDLVVVT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKFGVSEDCLYLNIYAPAHADIGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVHTFLGIPFAKPPVGPLRFAPPEAPEFWSGVRDGTAHPAMCLQN----LGVMKBIKLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPR----SQMHNWLDVLLFGLLLLLGHVQ-GQDSPEA-SPIRNTHTGQVRGSLVHVKDTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPQGLTSSASQWCFFLI--LQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPV
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Stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Staroa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.1%; Score 1266.5; DB 2;
47.1%; Pred. No. 5.3e-88;
tive 76; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A. 99:16899-16903(2002)
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RS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Faramer A.A., Rubbin G.M., Hong L.,
RA Diatchenko L., Warusina K., Faramer A.A., Rubin G.M., Hong L.,
RA Biatchenko L., Warusina K., Toshiyuki S., Carninci P., Prange C.,
RA Biatchenko L., Warusina K.J., Toshiyuki S., Carninci P., Prange C.,
RA Biatchenko L., Worley R.D., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Ra Bosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Ra Bosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Ra Hohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Willalion D.K., Malah A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ra Willian M., Madan A., Young A.C., Shevchenko Y., Buuffard G.G.,
Ra Hohes S.J., Marra M. A., Schmutz J., Myers R.M., Butterfield Y.S.,
Ma Jones S.J., Marra M.A., U., Smailus D.E., Schnerch A., Schein J.E.,
Ma Jones S.J., Marra M.A., U., Smailus D.E., Schnerch A., Schein J.E.,
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Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: Belongs to the type-B carboxylesterase/!
EMBL; BC074230; AAH74330.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                        Richardson
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                MEDLINE=22341132;
                                                                                                                                                                                               initiative.
                                                                                                                                                                                                   "Genetic and genomic tools initiative.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Battachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOC443703 protein (Fragment).
Name=LOC443703;
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Q6GM54;
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                                                                                                                                                                                                                                                       .L., Strausberg
                                                                                                                                FROM N.A.
                                                                                                                                                                      225:384-391 (2002)
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                                                                                                                                                                                                                                                     PubMed=12454917; DOI=10.1002/dvdy.10174; sberg R.L., Wagner L., Pontius J., Clifto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                            Xenopus
                                      carboxylesterase/lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568
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                                                                                                                                                                                                                                                     Clifton S.W.,
                                                                                                                                                                                                          NIH Xenopus
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PRESULT ORESULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 8 8 8 8 8
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Best Local S
Matches 258
O70177 PRELIMINARY; PRT; 561 AA.
070177;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
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InterPro; IPR000379; Ser_estrs.
Pfam; PP00135; COGSTECTES; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                    Rattus norvėgicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                             Name=carboxylesterase;
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436 VY	381 LHI : 376 LAL	322 GA 316 GV	264 PY : 260 LF	205 QV 200 QV	145 PV 	90 LR :- 83 VR	30 TG 23 TG	Query Match Best Local Similarity Matches 265; Conservat	thiolesterase B (EC 3) pro C;Species: Anas platyrhynchos (C C;Species: O5-May 1995 #sequence_re C;Accession: A47162 C;Accession: A47162 R;Hwang, C.S.; Kolattukudy, P.E. J. Biol. Chem. 268, 14278-14284, A;Title: Molecular cloning and (A;Reference number: A47162; MUII A;Reference number: A47162; MUII A;Residues: 1-557 <hwa> A;Residues: 1-557 <hwa> A;Cross-references: UNIPROT:Q04-C;Superfamily: cholinesterase; C;Keywords: hydrolase F;56-545/Domain: cholinesterase</hwa></hwa>	1	586 581.5 572.5 570.5 570.5 569.5 569.5 562.5 557.5
FYBFRHRP	SFKGA	FFPNEPLD	PYLEAHDYEK : : LFTEQP	AALSWVQK : : AALQWIQE	'LVWFPGGA FVWIHGGG	REATSYPNL : : RDAASYPPM	;PSAEGPQR : ;QKAEQPEV	ilarity Conserv	(EC 3 platyrhy platyrhy platyrhy platyrhy plattuku folloniar (1427 ar cloni er: A471 1162 1162 mRNA 77 <hwa> hels: UNIP hels: UNIP hels: UNIP hels: UNIP cholinest choline</hwa>		19.0 118.9 118.5 118.5 118.5 118.5 118.3
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)AFVKADHADEVRFVFGGAF	EYFHDKHSLTEIRDSLLDL 	AIPSIIGVNNHECGFLLP- : :: AVPYIIGVNNCEFGWILPR	HFCGNNASDSEALLRCLRT	PSSVTIFGESAGAISVSSL 	FDGSALAAYEDVLVVVVQY ::: : : YDGSALAAFDNVVVVTIQY	LREATSYPNLCLQNSEWLLLDQHMLKVHYPKF 	KGYQVKVNAAERSVNVFLGLPF	Score 1298.5; DB 2 Pred. No. 4.1e-94; 79; Mismatches 177;	sor - malla ard) ion 05-May 93 93 encing of t 300823; PM 300823; PM GB:L05493; inesterase ology <che:< td=""><td>ALIGNMENTS</td><td>\$47639 \$251433 \$511433 \$137254 \$137254 \$1731783 \$16236 \$131783 \$156690 \$131783 \$156690 \$27782 \$27782</td></che:<>	ALIGNMENTS	\$47639 \$251433 \$511433 \$137254 \$137254 \$1731783 \$16236 \$131783 \$156690 \$131783 \$156690 \$27782 \$27782
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A;Residues: 1-532 <0ZO>
A;Cross-references: UNIPROT:P14943
A;Cross-references: UNIPROT:P14943
C;Superfamily: cholinesterase; cholinesterase }
C;Keywords: carboxylic ester hydrolase
F;32-517/Domain: cholinesterase homology <CHE>
F;301,430/Active site: Ser, His #status predict
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Best Local Similarity
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                         ARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                        QHRPSFTKDLRPPHVRADHGDEVVFVFRSHLFGSKVPL----TEEEELLSRRVMKYWANF
                                                                                                                                             HIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEF
                                                                                                                                                                                                                                                                                                  NIAHFGGNPGRVTIFGESAGGTSVSSHVLSPMSQGLFHGAIMESLVALLPGLITSSSEVV
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                                                                                                                                                                                                                                                                                                                                                                               FKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQK
                                                                                     RHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKYWATF
                                                                                                                                                                                                         QKAFKAIPSIIGVNNHECGFLLP------MKEAPEILSGSNKSLALHLIQNIL
                                                                                                                                                                                                                                       S--TVVANLSRCGQVDSETLVRCLRAKSEEEMLAITQVFMLIPGVVDGVFLPRHPEELLA
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                                                                                                                                                                                                                                                                                                                            NIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKS
                                                                                                                    --PPALGDLLMDEYMGSNEDPKHLMAQFQEMMADAMFVMPALRVAHLQR-SHAPTYFYEF
                                                                                                                                                                               LADFOPVPSIIGINNDEYGWIIPKLLLAIDPQEERDRQAMREIMHQATKQLML-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            PNLCLQNSEWILLDQHMLKVHY--PKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIRNTHTGQVRGSLVHVEGTDAGVHTFLGIPFAKPPLGPLRFAPPEPAEAWSGVRDGTSL
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                                                                                                                                                                                                                                                                                                                                                                                                                      PAMCLQN--LAIMDQDVLLLHFTPPSIPMSEDCLYLNIYSPAHAREGSDLPVMVWIHGGG
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47.8%; Pred. No. 7.2e-89;
tive 76; Mismatches 167;
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A;Gene: GDB:CES2; iCE; CE2
A;Cross-references: GDB:9959011
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;58-544/Domain: cholinesterase homology <CHE>
F;15-95,123-280,291-428/Disulfide bonds: #status predicted
F;111,276/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;228,457/Active site: Ser, His #status predicted
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A;Residues: 1-559 <SCH>
A;Residues: 1-559 <SCH>
A;Cross-references: UNIPROT:000748; GB:Y09616; NID:g2058317; PIDN:CAA70831.1; PID:g205831
A;Experimental source: intestine
C;Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A;Title: Molecular cloning and characterization of a novel putative carbo: A;Reference number: JC5408, MUID:97289502; PMID:9144407
A;Accession: JC5408
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C;Species: Homo sapiens (man)
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC5408
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Best Local
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NFARNGNPNGEGLPHWPLFDQEEQYLQLNLQPAVGRALKAHRLQFWKKALP
                           TFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                                                                                         EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                                                                                                                                    FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
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                                                                                       EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF
                                                                                                                                                                     LLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY 436
                                                                                                                                                                                                                 ILHIPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY 439
                                                                                                                                                                                                                                                          FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT 377
                                                                                                                                                                                                                                                                                                                                               LIA----SSADVISTVVANLSACDQVDSEALVGCLRGKSKEEILAINKPFKMIPGVVDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                     VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY 265
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\$47655

Carboxylesterase (EC 3.1.1.1) precursor - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_C;Accession: \$47655

#text_change

09-Jul-2004

RESULT 4

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A;Molecule type: mRNA
A;Residues: 1-561 <SON>
A;Crose-references: UNIPP
C;Superfamily: cholinesto
C;Keywords: carboxylic es
F;58-546/Domain: cholines
F;227,459/Active site: S6
Carboxylesterase (BC 3.1.1.1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34607
R;Aida, K; Moore, R; Negishi, M.
Biochim. Biophys. Acta 1174, 72-74, 1993
A;Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase A;Reference number: S34607; MUID:93326638; PMID:7916639
A;Accession: S34607
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <AID>
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g40438
C;Keywords: Carboxylic ester hydrolase
C;Keywords: Carboxylic ester hydrolase
F;46-536/Domain: cholinesterase homology <CHE>
                                                                                                                                                                                                                                                                                                                                      RESULT
S34607
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Biochim. Biophys. Acta 1207, 138-142, 1994
A;Title: Cloning and sequence analysis of a hamster liver cDNA encoding a A;Reference number: S47655; MUID:94318665; PMID:8043605
A;Accession: S47655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHQSSFIKNKDARPSHVRADHGDHVAFVFGSDFWGLKIDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHRPQCF--EDTKPAFVKADHADEVRFVFGGAF--LKGDIVMFEGATEEEKLLSRKMMKY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELLASVDFHPVPSIIGVDSDECGWGVPLFMGLDHVIKNITRETLPAFLKSRAEHMM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDGTSEPAMCLQTDFMRPQISKERKIILPTISMSEDCLYLNIYTPAHAHEGSNLPVMVWI 145
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                                                                 PID:g404389
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F;215,443/Active site: Ser, His #status predicted
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RESULT 6
A39060
Carboxylesterase (EC 3.1.1.1) precursor - mou.
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar
C;Accession: A39060
R;Ovnic, M.; Tepperman, K.; Medda, S.; Elliot:
Genomics 9, 344-354, 1991
A;Title: Characterization of a murine cDNA en
A;Reference number: A39060; MUID:91169540; PM
                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 < CVNN>
A;Residues: 1-554 < CVNN>
A;Cross-references: UNIPROT:P23953; GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854
A;Cross-references: UNIPROT:P23953; GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
E;50-540/Domain: cholinesterase homology < CHE>
                                                                                                                                                                                                                       A; Accession: A39060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGPLRFSAPLPPQPWEGVRDASINPPMCLQDVERMSNSRFTLNEKMKIFPISEDCLTLNI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPEATEEEKQLSLTMMAQWSQFARTGNPNGKGLPPWPQLNQLEQYLEIGLEPRTGVKLKK 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLL-----PMKE-A 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAISQSGVVISKILE--DLNAWSEAQNFANSVACG-SASPAE-LVQCLLQKEGKDLITKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRLQFWTETLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRVDFWTSTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLIFSKYLQDAGCPVFLYEFQHTPSSFAKFKPAWVKADHSSENAFVFGGPFLTDESSLLA
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 37.8%; Score 1163; DB 2;
44.3%; Pred. No. 1.9e-83;
tive 84; Mismatches 193;
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Pred. No. 2.7e-85;
31; Mismatches 183;
                                                                                                                                                                                                                                                                                              Elliott,
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PMID:1840565
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16 LILQPILGHRQWGKTGBSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGS

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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecules: 19-40 <MAT2>
A;Rolecules: 19-40 <MAT2>
A;Rolecules: 19-40 <MAT2>
A;Rolecules: 19-40 <MAT2>
A;Rolecules: 19-40 <MAT2>
A;Rolecules: 19-40 <MAT2>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-566/Product: carboxylesterase #status experimental <MAT>
F;51-552/Domain: cholinesterase homology <CHB>
F;51-552/Domain: cholinesterase homology <CHB>
F;61-552/Domain: cholinesterase homology <CHB>
F;61-652/Domain: cholinestera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxylesterase (EC 3.1.1.1) precursor - pig N,Alternate names: proline-beta-naphthylamidase C,Species: Sus scrofa domestica (domestic pig) C;Date: 04-Dec-1992 #sequence_revision 04-Dec-19 C;Accession: S19307, S23607 R;Matsushima, M.; Inoue, H.; Ichinose, M.; Tsuka FEBS Lett. 293, 37-41, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEBS Lett. 293, 37-41, 1991
A;Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-r
A;Reference number: S19307; MUID:92070571; PMID:1959668
A;Accession: S19307_____
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q29550; A;Accession: S23607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-566 < MAT1>
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                                                                                                                                                                                                 ;19-566/Product: Carboxylesterase #status experimental <;51-552/Domain: cholinesterase homology <CHE>;80/Binding site: Carbohydrate (Asn) (covalent) #status;222,467/Active site: Ser, His #status predicted
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                                                                                                                                       Similarity
                                                    WCFFLIIQPLIGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
  WILLPLVITSLASSATW--AGQPASPPVVDTAQGRVLGKYVSLEGLAQPVAVFLGVPFAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEKLLSRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRSLRDAGVSTYMYEFRYRPSFVSDKRPQTVEGDHGDEIFFVFGAPLLK-----EGASE
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                                                                                                                                     37.8%;
44.3%;
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                                                                                                        Score 1162.5; DB Pred. No. 2.1e-83; 1; Mismatches 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: X63323; NID: g1930;
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                                                                                                        Indels
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J. Biochem. 104, 801-806, 1988

A;Title: Molecular cloning and nucleotide sequence of cDNA of micro A;Reference number: JX0054; MUID:89174514; PMID:3235453

A;Accession: JX0054

A;Molecule type: mRNA

A;Residues: 1-549 <TAK>
A;Experimental source: liver

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: carboxylic ester hydrolase; glycoprotein; microsome

F;10-549/Product: carboxylesterase E1 #status predicted <MGT>
F;00-538/Domain: signal sequence #status predicted <MGT>
F;00-538/Domain: cholinesterase homology <CHE>
F;79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #s
                                                                                                                                                                                                                                                                                                                                                                                                            carboxylesterase (EC 3.1.1.1) El precursor, minor form - C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_C;Accession: JX0054 C;Accession: JX0054 R;Takagi, Y; Morohashi, K; Kawabata, S.; Go, M.; Omura, J. Biochem. 104, 801-806, 1988
         Query Match
Best Local S
Matches 238
                                                                                                :221,453/Active site: Ser, His #status predicted
                             Local Similarity
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         Conservative
                           37.2%; Score 1144; DB 2; 43.5%; Pred. No. 5.8e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----APEEEVSLSKTVMKFWANFARSGNPNGEGLPHWPMYDQEEGYL
92;
         Mismatches
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129
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                                                                                                                         11 LAVCPIWGH-----PSSP-PVVDTTKGKVLGKYVSLEGFTQPVAVFLGVPFAKPPLGS
YLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGF
                                                                              LRFTNPQPASPWDNLREATSYPNLCLQN-----SEWLLLDQHMLKVHYPKFGVSEDCL 128
                                                                                                                                                                LILOPLIGHROWGKTGPSAEGPORNTRIGWIOGKOVTVLGSPVPVNVFLGVPFAAPPLGS
                                        LRFAPPEPAEPWSFVKNTTTYPPMCSQDGVVGKLLADMLSTGKESIPLEF----SEDCL
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                      Gaps
  188
                                        117
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A, Molecule type: mRNA
A; Residues: 61-567 < LON>
A; Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A; Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
R; Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
Genomics 17, 76-82, 193
A; Title: Molecular cloning and characterization of a human carboxylesterase gene.
A; Reference number: A47376; MUID:94010913; PMID:8406473
A; A; Residues: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; References: GB:D21088; NID:g45476; PIDN:BAA04650.1; PID:g458470
A; Residues: 1-3, 'PALV', '8-11, 'A', '13-567 < SHI>
A; Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase-A; Reference number: A49816; MUID:91300111; PMID:2070086
A; Molecule type: mRNA
A; Residues: 'G',65-185,'G',187-361,363-567 < ZSC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human N;Alternate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase (Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A41010, JH0327; A47376; A49816; PS0280; I61085; A48809; I57004 R;Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A. J. Biol. Chem. 266, 18832-18838, 1991 A;Biol. Chem. 266, 18832-18838, 1991 A;Title: A serine esterase released by human alveolar macrophages is closely related A;Reference number: A41010; MUID:92011649; PMID:1918003 A;Accession: A41010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P23141; GB:M73499; NID:g179927; PIDN:AAA35649.1; PID:g179928 A;Note: parts of this sequence, including the amino end of the mature protein, were conf R;Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R. Life Sci. 48, PL43-PL49; PA149-PL49; PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149-PA149
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A; Residues: 1-567 < MUN>
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Best Local Similarity
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A;Map position: 16q13-16q22.1
c;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic seter hydrolase; endoplasmic ret
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-145/Domain: propeptide #status predicted <PRO>
F;19-553/Domain: cholinesterase homology <CHE>
F;146-567/Product: carboxylesterase #status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X52973; NID:g36421; PIDN:CAA37147.1; PID:g1335304 R;Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M. Gene 108, 289-292, 1991 Gene 108, 289-292, 1991 A;Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase. A;Reference number: PS0280; MUID:92084150; PMID:1748313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;146-567/Product: carboxylesterase #status experimental F;564-567/Region: endoplasmic reticulum retention signal F;221,468/Active site: Ser, His #status predicted
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A;Residues: 1-17,'A',18-55,'G',57-535,'G',537-567 <KRO2>
A;Cross-references: GB:L07764; NID:g180947; PIDN:AAA16036.1;
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Biochemistry 32, 11606-11617, 1993
A;Title: Glycosylation-dependent activity of baculovirus-expressed human A;Reference number: A48809; MUID:94032283; PMID:8218228
A;Accession: 161085
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A;Residues: 114,'H', 116-280,'A',282-300,'IGNSYLWTYRETQREST',318-336,'R',338-382,'GSPI',38
A;Cross-references: GB:M65261; NID:g187028; PIDN:AAA83932.1; PID:g187029
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A; Accession: PS0280
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A;Residues: 1-55,'G',57-361,363-535,'G',537-567 <KRO1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 LNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFF 189
LFLDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGDELFSV
                                             SLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFV
                                                                                                                                                                                                                                                                                                                                                          TLSQKTKSFT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLGPLRFTPPQPAEPWSFVKNATSYPPMCTQDPKAGQLLSELFTNRKENIPLKLSEDCLY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP 71
                                                                                                                                            GWLI PMQLMSYPLSEGQLDQKTAMSLLWKSYPLVCIAKELI PEATEKYLGGTDDTVKKKD
                                                                                                                                                                                                                                                                                      ETTLKMKFLSLDLQGDPRESQPLLGTVIDGMLLLKTPEELQAERNFHTVPYMVGINKQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFHKAIMESGVAIIPYLEAHDYEK--SEDLQVVAHFCGNNASDSEALLRCLRTKPSKELL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STGDEHSRGNWGHLDQVAALRWVQDNIASFGGNPGSVTIFGESAGGESVSVLVLSPLAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSE--WLLLDQHMLKVHYPKFGVSEDCLY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLRAFILATISASAAWGH--PSSP-PVVDTVHGKVLGKFVSLEGFAQPVAIFLGIPFAKP 58
                                                                                                                                                                                                             GFLLPMKEAPEILSGS--NKSLALHLION---ILHIPPOYLHLVANEYFHDKHSLTBIRD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                      LPHRAISESGVALTSVLVKKGDVKPLAEQIAITA---
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                                                                                                                                                                                                                                                                                                                                                          ----RVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHEC 352
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A;Residues: 1-6,'F',8-59,'P',61-212,'A',214-252,'T',254-309,'IT',312-341,'N',343-424,'FY
A;Residues: GB:U10697; NID:g562007
A;Note: the sequence in GenBank entry RNUI0697, release 107, (PID:g562008) has the codon R;Robbi, M.; Beaufay, H.
submitted to the EMBL Data Library, September 1994
A;Reference number: S49257
A;Accession: S49257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 19-48 <MOR>
A;Experimental source: liver
R;Yan, B; Yang, D; Brady, M; Parkinson, A.
J. Biol. Chem. 269, 29688-29696, 1994
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, A;Reference number: A55304; MUID:95050819; PMID:7961958
                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic c;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver F;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g550418
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: UNIPROT:Q64573; EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g5504
A;Experimental source: liver
R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Blochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal carboxylesterases
A;Reference number: S51202; MUID:95077430; PMID:7986098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62788; S51203; A55304; S49257
R;Robbi, M.; van Schaftingen, E.; Beaufay, H.
Biochem. J. 313, 821-816, 1996
A;Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal A;Reference number: S62788; MUID:96190723; PMID:8611161
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A; Residues: 1-561 < ROB>
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                                                                                                                                                                                                                                                                ;50-551/Domain: cholinesterase homology <CHE>;221,466/Active site: Ser, His #status predicted;301/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                       1-18/Domain: signal sequence #status predicted <SIG>
19-561/Product: carboxylesterase ES-4 #status experimental
                                                                                                                                                                                                                                                                                                                                                                                               Description: catalyzes conversion of carboxylic ester to alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA; Residues: 1-561 <RO2>
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                                SIRFAPPOPAEPWSFVKNTTTYPPMCSQDAAKGQRMNDLLTNRKEKIH---LEFSEDCLY
                                                                      SLRFTNPQPASPWDNLREATSYPNLCLQNSEW-----LLLDQHMLKVHYPKFGVSEDCLY
                                                                                                           FLILVSLATCVVYG--NPSSP-PVVDTTKGKVLGKYVSLEGVTQSVAVFLGVPFAKPPLG
                                                                                                                                           FLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLG
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43.4%;
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                                                                                                                                                                                         Score 1139; DI
Pred. No. 1.5e
82; Mismatches
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LSWVQKWIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEA
                                                          WIHGGGLVLGGASTYDGLVLSTHENVVVVVIQXRLGIWGFFSTGDEHSRGNWGHLDQVAA
                                                                                                                                                               REATSYPNICLQNSEWILLIQHMIKVHYPKFGV--SEDCLYINIYAPAHADTGSKLPVIV 148
                                                                              WFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAA
                                                                                                                                     KNATSYPPMCFODPVTGQIVNDLLTNRKEKIPLQFSEDCLYLNIYTPADLTKSDRLPVMV 138
                                                                                                                                                                                                                                        GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVVPLGVPFAAPPLGSLRFTNPQPASPWDNL
                                                                                                                                                                                                              GHPSSPPMVDTVQGKVLGKYISLEGFTQPVAVFLGVPFAKPPLGSLRFAPPQPAEPWSSV 78
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                             37.0%;
                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                          Score 1138.5; DB 2;
Pred. No. 1.6e-81;
'6; Mismatches 195;
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APILR-----DGASEEEIKLSKMVMKFWANFARNGNPNGRGLPHWPQYDQKEEYLQIGA 529
                                                                                                                                                                           LDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFG
                                                                                                                                                                                                                                                                                                                  MKWWNLIKLSSQRDNKESYHFLSTVVDNVVLPKDPKEILAEKNFNTVPYIVGINKQECGW
                                                                                  GAFLKGDIVMFEGATEEEKLLSRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDL 529
                                                                                                                                                                                                                                                                  LLP--MKEAPEILSGSNKSLALHLIQ---NILHIPPQYLHLVANEYFHDKHSLTEIRDSL
                                                                                                                                  LAFIGDVSFSIPSVMVSRDHRDAGAPTYMYEYQYYPSFSSPQRPKHVVGDHADDLYSVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLPTMMGFVPADVE-LDKKMAITLLEKFASLYGIPEDIIPVAIEKYRKGSDDSIKIRDGI
                                                                                                                                                                                                                                                                                                                                                             SQKTK-----SFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGF
                                                                                                                                                                                                                                                                                                                                                                                                           LFHRAISESGVVFLPGLLTKDVRPA--AKQIADMAGCETTTSAIIVHCLRQKTEEELLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STGDEHSRGNWGHLDQVAALHWVQDNIANFGGDPGSVTIFGESAGGFSVSVLVLSPLTKN
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Carboxylesterase (EC 3.1.1.1) egasyn - mouse

N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-;

C;Species: Mus musculus (house mouse)

C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004

C;Accession: A55281

R;Ovnic, M; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.; (
Genomics 11, 956-967, 1991

A;Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-;
A;Reference number: A55281; MUID:92147141; PMID:1783403

A;Accession: A55281

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Rolecule type: mRNA; protein

A;Rote: sequence extracted from NCBI backbone (NCBIN:80191, NCBIP:80194)

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum

F;51-552/Domain: cholinesterase homology - CHE>

F;222,467/Active site: Ser, His #status predicted

2

Indels Length

29;

Gaps

208 198

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A;Cross-reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT:P10959; GB:M20629; GB:X13587; NID:g203279; C; Superfamily: Cholinesterase; Cholinesterase homology C; Keywords: carboxylic ester hydrolase; glycoprotein P;1-9/Domain: signal sequence #scatus predicted <SIG> F;10-540/Product: carboxylesterase homology <CHE> F;41-529/Domain: cholinesterase homology <CHE> F;41-529/Domain: cholinesterase homology <CHE> F;70,285,266,293,366,467/Binding site: carbohydrate (Asn) (covalent) F;212,444/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxylesterase (EC 3.1.1.1) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                   LAVCPIWGH-----PSSP-PVVDTTKGKVLGKYVSLEGFTQPVAVFLGVPFAKPPLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSRKMMKYWATFARTGNPNGNDLSLWPAYNLTBQYLQLDLNMSLGQRLKEPRVDFWTSTI 549
                                             LSQK--TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPBILS 366
                                                                              NLFHRAISESGVVLTTNLDKKNTQAV--AQMIATLSGCNNTSSAAMVQCLRQKTBABLLE
                                                                                                           GLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLT 308
                                                                                                                                                                      FTTWDQHAPGNWAFKDQVAALSWVQKNIBFFGGDPSSVTIFGESAGAISVSSLILSPMAK 248
                                                                                                                                                                                                       YLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGF 188
                                                                                                                                                                                                                                                                     LRFAPPEPAEPWSFVKNTTTYPPMCSODGVVGKLLADMLSTGKESIPLEF----SEDCL
                                                                                                                                                                                                                                                                                                  LRFTNPQPASPWDNLREATSYPNLCLQN-----SEWILLDQHMLKVHYPKFGVSEDCL 128
                                                                                                                                                                                                                                                                                                                                                              LILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMSLLKKSSFLLNLPEDAIAVAIEKYLRDKDYTGRNKDQLLELIGDVVFGVPSVIVSRGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALHLION---ILHIPPOYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYH
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                                                                                                                                          FSTGDEHSRGNWAHLDQLAALRWVQDNIANFGGNPDSVTIFGESAGGVSVSALVLSPLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDAGAPTYMYEFQYSPSFSSEMKPDTVVGDHGDEIYSVFGAPILRG-----GTSEEEIN
                 LTVKLDNTSMSTVIDGVVLPKTPEEILTEKSFNTVPYIVGFNKQEFGWIIPTMMGNLLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSKMMKFWANFARNGNPNGQGLPHWPEYDQKEGYLQIGATTQQAQKLKEKEVAFWTELL
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                             36.9%; Score 1136; DB 2;
43.3%; Pred. No. 2.4e-81;
ative 91; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:X13587; NID:g203279;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 540;
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A;Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver F;1-18/Domain: signal sequence #status predicted <SIGs F;19-561/Product: carboxylesterase #status predicted <MAT> F;50-551/Domain: cholinesterase homology <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Yan, B.; Yang, D.; Parkinson, A. Arch. Biochem. Biophys. 317, 222-234, 1995
A;Title: Cloning and expression of hydrolase C, a member A;Reference number: S71597; MUID:95177656; PMID:7872788
A;Accession: S71597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: hydrolase C
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C;Accession: S71597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;558-561/Region: endoplasmic reticulum retention signal F;79,301/Binding site: carbohydrate (Asn) (covalent) #st F;221.466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-561 < YAN>
A; Experimental source:
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxylesterase (EC 3.1.1.1) precursor, liver N;Alternate names: hydrolase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
NKSLALHLIQ---NILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REATSYPNICLQNSEW-----LLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                                                                                                                                                                                                                               VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY
                                                     ESYHFLSTVIDDVVLPKDPKEILAEKNFNTVPYIVGINKQECGWLLPTMMRFVPPDVK-L
                                                                                                          S----FTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP--MKEAPEILSGS
                                                                                                                                                                                                                       LEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQK-----TK 314
                                                                                                                                                                                                                                                                                  VAALHWVQDNIANFGGDPGSVTIFGESAGGFSVSVLVLSPLSKNLYHRAISESGVVLITQ
                                                                                                                                                                                                                                                                                                                                                                                                VMVWIHGGGLTQGGASTYDGRVLSAYENVVVVAIQYRLGIWGFFSTGDEHSRGNWGHLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            VLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNTTTYPPMCSQDATKGQRMNDLLTNRKEKVH---LQFSEDCLYLNIYTPADFTKDSRMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNPSSPPVVDTMKGKVLGKYASLEGVTQSVAVFLGVPFAKPPLGSLRFAPPQPAEPWSFV
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                                                                                                                                                                     LFTKDVRPA--AKQIADMAGCKTTTSAIIVHCLRQKTEEELLEIMEKMNLIKLSSQRDTK
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43.4%; Pred. No. 8.3e-81;
tive 83; Mismatches 188;
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A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Mesidues: 503-554, %, 556-561 < MED>
A; Cross references: EMBL: X65295; NID: g57557; PIDN: CAA46390.1; PID: g57558
C; Superfamily: cholinesterase; cholinesterase homology
C; Koywords: carboxylic ester hydrolase; glycoprotein
F; 1-18/Domain: signal sequence #status predicted < MGIO>
F; 19-561/Product: carboxylesterase ES-3 #status predicted < MAT>
F; 50-551/Domain: cholinesterase homology < CHE>
F; 79,107,489/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 7221,466/Active site: Ser, His #status predicted
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A; Residues: 1-561 <ROB>
A; Residues: 1-561 <ROB>
A; Crose-references: UNIPROT: Q63108; GB: X81395; NID: g550146; PIDN: CAA57158.1;
A; Experimental source: liver
A; Experimental source: Liver
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C;Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_chanc
C;Accession: JC2447; 823462
R;Robbi, M.; Beaufay, H.
Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
A;Title: Cloning and sequencing of rat liver carboxylesterase
A;Reference number: JC2447; MUID:95032008; PMID:7945287
A;Accession: JC2447
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A;Title: The carboxylesterase family exhibits C-terminal
A;Reference number: $23460; MUID:92299008; PMID:1606962
A;Accession: $23462
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                                                                            VLSPLAKNLFHKAISESGVALTAGLVKKNTRPLAEKIAVVS--
                                                                                                                                                                                              RLGIWGFFSTGDEHSRGNWGHLDQVAALHWVQDNIDNFGGDFGSVTIFGESAGGESVSVL
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                   KPSKELLTLSQKTKSFT
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42.2%; Pred. No. 2.7e
tive 86; Mismatches
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2.7e-80;
ches 193;
               RVVDGAFFPNEPLDLLSQKAFKAIPSII
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                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 19-48 <MOR>
R;Medda, S.; Proia, R.L.

Eur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal sequence
A;Reference number: S23460; MUID:92299008; PMID:1606962
A;Accession: S23460
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-185,'Q',187-422,'M',424-505,'N',507-565 <MED>
A;Cross-references: EMBL:X65296; NID:g57553; PIDN:CAA46391.1; PID
B;Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
   C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; F;1-18/Domain: signal sequence #status predicted <SIG> F;19-565/Product: carboxylesterase #status predicted <MAT> F;50-551/Domain: cholinesterase homology <CHE> F;79,489/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                                                                                                                                          Biochem. J. 274, 693-697, 1991
A;Title: Purification and characterization of carboxylesterases
A;Reference number: S14361; MUID:91190080; PMID:2012599
                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 19-26, 'D', 28-37 < GAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X51974; NID:g56898; PIDN:CAA36236.1; PID:g56898; R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A. Arch. Biochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal A;Reference number: S51202; MUID:95077430; PMID:7986098
A;Accession: S51202
                                                                                                                                                                                                                                                    A; Accession: S14361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9R135; EMBL:X51974
A;Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found
A;Note: the sequence from Fig. 4 is inconsistent with that from
R;Robbi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. J. 269, 451-458, 1990
A;Title: Nucleotide sequence of cDNA coding for rat liver pIA;Reference number: S10367; MUID:90351366; PMID:2386485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change C;Accession: S10367; S12468; S51202; S23460; S14361 R;Robbi, M.; Beaufay, H.; Octave, J.N. Biochem. J. 269, 451-458, 1990
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S10367
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A; Residues: 1-264, 'K', 266-565 < ROB2>
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A; Residues: 1-565 < ROB1>
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                                                                                                         185 IFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILS 244
|:||:||:||:||:||:||:||
174 IWGFFSTGDEHSRGNWGHLDQVAALHWVQDNIANFGGNPGSVTIFGESAGGFSVSALVLS 233
 525
                                                       471 FSVFGSPFLK-----DGASEEETNLSKMVMKYWANFARNGSPNGGGLPHWPEYDQKEGY 524
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                                                                                                                                                                                                                                                                                        245 PMAKGLEHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSK 304
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                                                                                RFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQY 524
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Search completed: June 15, 2005, 09:39:49 Job time : 27 secs

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1 MPQGLTSSASQWCFFLILQP......PLSSLTFLSLLQPFFFFCAP 581
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ALIGNMENTS

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APPLICANT: CAUTLIS, ROTY A. J.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLS OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLS OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
TANGER OF SET SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-023-515-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 3079; DB 13; Length 581; Best Local Similarity 100.0%; Pred. No. 1.1e-277; Matches 581; Conservative 0; Mismatches 0; Indels 0;
61 NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLLDQHMLKVHYPK 120
                                                                                                                                                                                                                     1 MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV 60
1 MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV 60
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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERA
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERA
TITLE OF INVENTION: PAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT APPLICATION NUMBER: US/10/023,515
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2001-03-28
INMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
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Matches 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10674636
Publication No. US20040086922A1
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                                                                               1 MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
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                                                                                                                                              Similarity
                 NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLLDQHMLKVHYPK 120
MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
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                                                                                                                                Conservative
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                                                                                                                           Score 3079; DB 15;
Pred. No. 1.1e-277;
; Mismatches 0;
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APPLICANT: SAILUREL, VELNALEMATIO

APPLICANT: Eliasof, Scott D.

FITLE OF INVENTION: URCLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884, 11712 OF INVENTION: URCLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884, 11712 OF INVENTION: 1405, 635, 4421, 5410, 30905, 2045, 16405, 18560, 2047, 171712 OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164, 71712 OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675, 171712 OF INVENTION: 32720, 4809, 143,03, 16816, 17827, 32620, 577, 619, 1423, 171712 OF INVENTION: 2543, 8263, 15402, 16287, 30911, 41897, 1643, 171712 OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

FILTE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

FILTE OF INVENTION: UNMER: US/10/757,262

CURRENT APPLICATION NUMBER: US 60/440, 318

PRIOR APPLICATION NUMBER: US 60/440, 318

PRIOR FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: US 60/440, 338

PRIOR APPLICATION NUMBER: US 60/440, 783

PRIOR APPLICATION NUMBER: US 60/457, 901

PRIOR APPLICATION NUMBER: US 60/457, 901

PRIOR APPLICATION NUMBER: US 60/457, 901

PRIOR APPLICATION NUMBER: US 60/458, 775

PRIOR APPLICATION NUMBER: US 60/457, 901

PRIOR APPLICATION NUMBER: US 60/458, 775

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PRIOR APPLICATION NUMBER: US 60/478, 742

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Publication No. US20040197825A1
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APPLICATION NUMBER: US 60/499,594
FILING DATE: 2003-09-02
APPLICATION NUMBER: US 60/506.332
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97, 1643,
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
APPLICANT: SMITHKLINE BEECHAM p.l.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: E07/US01/49232
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR PILING DATE: 2000-12-0
PRIOR APPLICATION NUMBER: 60/260,482
                                                                                                                                                                                                                           RESULT 4
US-10-451-168-91
Sequence 91, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
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RESULT 5 US-10-433-256-10

Sequence 10, Application US/10433256
Publication No. US20040081980A1
GENERAL INFORMATION:
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: AVIZU, Chandra S.; RING, Huijun Z.
APPLICANT: LEE, Ernestine A.; DING, Li

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; SEQ ID NO 91
LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-91
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PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-02-06
PRIOR FILLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILLING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILLING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/889,622
PRIOR FILLING DATE: 2002-06-28
PRIOR FILLING DATE: 2002-06-28
PRIOR FILLING DATE: 2002-06-28
PRIOR FILLING DATE: 2002-06-28
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Similarity 97.0%;
ILSASDMLHSPLSSLTFLSLLQPFFFFFCAP 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLLDQHMLKVHYPKFGVSEDCLYLN
                                                                            RKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                                                                                     AGAPVYFYBFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLS
                                                                                                                                                                                                  LALHLIQNILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRD
                                                                                                                                                                                                                                             KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
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                                                             RKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                                                                                                                                                 LALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRD
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Pred. No. 2.1e-262;
3; Mismatches 6;
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APPLICANT: GRAPH, MALINGER N.; NGUYMES
APPLICANT: ISON, Craig H.
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0313 USN
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2001-12-08
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR PILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL PROGRAM
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 642
; TYPE: PAT
; ORGANISM: Homo sapiens
; FEATURE:
; PANE/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 6538080CD1
US-10-433-256-10
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Best Local Similarity
Matches 548; Conserv
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                     DLSLWPAYNLTEQYLQLDLMMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS 570
                                                                                                                  TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEBEKLLSRKMMKYWATFARTGNENGN
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YUE, Henry; TRIBOULEY, Catherine M.
LU, Dyung Aina M.; LAL, Preeti G.
WARREN, Bridget A.; YANG, Junming
CHAWLA, Narinder K.; NGUYEN, Danniel B.
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nilarity 99.5%;
Conservative
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Pred. No. 6.3e-261;
2; Mismatches 1;
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US-10-451-168-92
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CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: E07/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PRIOR DATE: 2000-12-19
PRIOR PRIOR PAPLICATION NUMBER: 60/257,704
PRIOR PPLICATION NUMBER: 60/257,048
PRIOR PPLICATION NUMBER: 60/260,482
PRIOR PILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PRIOR DATE: 2001-01-09
PRIOR PPLICATION NUMBER: 60/266,797
PRIOR PPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
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; Publication No. US20040091969A1
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SOFTWARE: FastSEQ for
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
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TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: GP50039
                                                                                                                                                     246 HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499;
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KSLAL-----HLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALI
                                                                                 KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKE--APEILSGSN 369
                                                                                                                                                                                      HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSBALLRCLRTKDSKELLTLSQ 311
                                                                                                                                                                                                                                                             WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                                                                                                                                                                                                                                                                                         WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDDSSVTIFGESAGAISVSSLILSPMAKGLF 251
                                                                                                                                                                                                                                                                                                                                                               IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT 185
                                                                                                                                                                                                                                                                                                                                                                                             IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHWLKVHYPKFGVSEDCLYLN 131
                                                   KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMVRILAVHTATPSN
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Gaps

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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
TILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF ESQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEC ID NOS 2375
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2375
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Sequence 2375, Application US/10094749
Publication No. US20030219741A1
                                                                                                                                                                                                                                                Query Match 84.6%;
Best Local Similarity 90.9%;
Matches 501; Conservative
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
                                                                                                                                       REATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF 150
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NAGAI, KEIICHI
IRIE, RYOTARO
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WVQKNIEFFGGDESSVIIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEAHD
                                                                                                                 REATSYPHICLONSEWILLIDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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                                                                    PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTTWDQHAPGNWAFKDQVAALS
                                                 PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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Pred. No. 1.2e-233;
0; Mismatches 0;
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US-10-114-270-196
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               CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
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APPLICANT: Rothenberg, Mark B.
TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids
FILE REFERENCE: 21402-322C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
     APPLICATION NUMBER: 60/281,906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Guo, Xiaojia
: Kekuda, Ramesh
: Miller, Charles E.
: Malyankar, Uriel M.
: Spytek, Kimberly A.
: Patturajan, Meera
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Shimkets, Richard A.
Gangolli, Bsha A.
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Burgess, Catherine E.
Gerlach, Valerie
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Gorman, Linda
Shenoy, Suresh G.
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                                                                                                                                                                                                                                                                                                               Taupier Jr., Raymond J. Casman, Stacie J.
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                                                                                                                                                                                                                                                                                                Ji, Weizhen
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                                                                                                                                                                                                                                                                                    Anderson, David W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vladimir Y.
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                                                                                                                                                                    Encoding
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Same

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RESULT 9
US-10-381-898-2
US-10-381-898-2
Sequence 2, Application US/10381898
Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda, BAUGHN, Mariah R.;
APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: BOROWSKY, Mark LLIOTT, Vicki S.;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GAUDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
KHAN, Farrah A.; LAL, Preeti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR REPLICATION NUMBER: 60/282,930
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR RILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR PPLICATION NUMBER: 60/283,710
PRIOR PPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR PILING DATE: 2001-04-17
Remaining Prior Application data remove
NUMBER OF SEQ ID NOS: 470
FRICTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-270-196
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                                                                                                                                                                                                                                                                                      TGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
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ilarity 94.3%;
Conservative
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Pred. No. 8.7e-233;
4; Mismatches 17; I
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CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US01/30662
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-26
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEG ID NOS: 36
SOFTWARE: PERL PROGRAM
SEG ID NO 2
LENGTH: 618
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Best Local (
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No
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APPLICANT: ARVIZU, Chandr;
APPLICANT: ARVIZU, Chandr;
APPLICANT: SANJANWALL, Mac
APPLICANT: SANJANWALL, Mac
APPLICANT: CHANGLA, Marind;
APPLICANT: WARREN, Bridget
APPLICANT: WARREN, Bridget
APPLICANT: YANG, Junming;
TITLE OF INVENTION: ENUG ME
FILE REFERENCE: PI-0233 US)
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ARVIZU, Chandra S.; POLICKY, Jennifer L.;
RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
SANJANWALA, Madhusudan M.;
TANG, Y. Tom; TRIBOULBY, Catherine M.;
CHAWLA, Narinder K.; WALSH, Roderick T.;
WARREN, Bridget; XU, Yuming;
YANG, Junming; YAO, Monique; YUE, Henry
INVENTION: DRUG METABOLIZING ENZYMES
TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEBEKLLSRKMMKYWATFARTGNDNGN
                                                              VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAFVYFYEFRHRPQCFED
                                                                                     VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED
                                                                                                                                                                         DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPBILSGSNKSLALHLIQNILHIPPQYLHL
                                                                                                                                                                                                                                                    YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL 330
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                                                                                                                                                                                                                              YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
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Pred. No. 6.6e
1; Mismatches
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RESULT 11
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US-10-104-047-2219
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Sequence 2, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY
PILE REFERENCE: SHIG PP02US006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 2219
LENGTH: 469
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TITLE OF INVENTION: NO. US20030236392A1el full length
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
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Local Similarity 99.6%;
hes 467; Conservative
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                                                                                                                                                                                                                                                                                LKGDIVMFEGATEEEKLLSRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEFLDLLSQKAFKAIPSIIGVNSHEC
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                                                                                                                                                                                         <u>LKGDI VMPEGATEEEKLLSRKMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS</u>
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Pred. No. 1.5e-219;
2; Mismatches 0;
                   DISEASE MARKER
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LENGTH: 542
TYPE: PRT
ORGANISM: Felis o
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 501
              510 NDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTI
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                                                                                                                                                                     GDERKKDLQVLARICGCHASDSAALLQCLRAKPSEELMDISKKLTFSIPVIDDFFFFDEP
                                                                                                                                                                                                                                                                                                      EGVPLWPAYTQSEQYLKLDLSVSVGQKLKEQEVEFWMNTI
                                                               DTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNG
                                                                                                    LVADHYFYNKHSPVEIRDSFLDLLGDVLFVVPGVVTARYHRDAGAPVYFYEFQHPPQCLN
                                                                                                                        LVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFE
                                                                                                                                                      VALLTQKAFNSVPSIIGVNNHECAFLL-STEFSEILGGSNRSLALYLVHTFLNIPTQYLH
                                                                                                                                                                                                                      DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEP
                                                                                                                                                                                                                                                        WVRDNIEFFGGDPRSVTIFGESAGAISVSSLILSPIANGLFHKAIMESGVAILPLLMRPP
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US-10-233-933A-4

Sequence 4, Application US/10233933A

Publication No. US20040214171A1

GENERAL INFORMATION:

APPLICANT: Yamashita, Tetsuro
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masso

TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006

CURRENT APPLICATION NUMBER: US/10/233,933A

CURRENT APPLICATION NUMBER: US/10/233,933A

CURRENT FILING DATE: 2002-09-03

PRIOR APPLICATION MESER: JP2002-057908

PRIOR FILING DATE: 2002-04-03

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

LENGTH: 542

TYPE: PAT

ORGANISM: Felis catus

US-10-233-933A-4

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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-7,048
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/260,482
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Sequence 93, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.1.c.
              PRIOR
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Best Local Similarity
Matches 373; Conserv
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PRIOR
NUMBER
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                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GP50039
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                       OR FILING DATE: 2001-01-09
OR APPLICATION NUMBER: 60/264,922
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: 60/266,797
OR FILING DATE: 2001-02-06
OR APPLICATION NUMBER: 60/276,988
                            APPLICATION NUMBER: 60/289,622
                                                             APPLICATION NUMBER: 60/281,535
                                            FILING DATE: 2001-04-04
                                                                             FILING DATE: 2001-03-19
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              2002-06-28
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals ar
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals ar
US-09-925-298-689
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US-09-925-298-689
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; SEQ ID NO 93
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO3
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 689
LENGTH: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 689, Publication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                 Similarity
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 GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV
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D. US20020039764A1
                                                              39.9%; Score 1230; I ilarity 46.7%; Pred. No. 2.66 Conservative 91; Mismatches
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                                                                0; DB 9;
2.6e-105;
ches 168;
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 689, Application US/10102806 Publication No. US20030054421A1 GENERAL INFORMATION:
                                                                                                  Query Match 39.9%; Score 1230; DB 14; Best Local Similarity 46.7%; Pred. No. 2.6e-105; Matches 248; Conservative 91; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 846
SOPTWARE: PatentIn Ver. 2.
SEQ ID NO 689
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo :
FEATURE:
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REATSYPNLCLQN-----SEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
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                                                        EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEGQLSRKMMKYWA
                                                                                   EFRHRPOCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWA 499
                                                                                                                      LLMLPPTFGDLLREBYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY
                                                                                                                                                  ILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                                                                FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT
                                                                                                                                                                                              FFPNBPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPĒILSGSNKSLALHLIQN
                                                                                                                                                                                                                                                                      LEAHDYEKSEDL--QVVAHFCGNNASDSBALLRCLRTKPSKELLTLSQKTKSFTRVVDGA 323
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Search completed: June 15, 2005, 09:46:09
Job time: 88 secs

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Result
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-Q=/Cgn2 1/USPTO spool/664091/runat 14062005_133640_10451/app_query.fasta_1.775
-Q=/Cgn2 1/USPTO spool/664091/runat 14062005_133640_10451/app_query.fasta_1.775
-DB=M_Genneseq_1650ec04 -QFWT=fastap_SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM=sxt -HABAFIXE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6664091_@CGN_1_1_470_@runat_14062005_133640_10451 -NCPU=6 -ICPU=3
-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=170 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                              Score
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: geneseqn1980s:*
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ARRESULT 1 ARBHAGAZ ID ARBNA XX ARBNA XX ARBNA DI 23-5 XX Cark KW Cark KW Cirk KW Cirk KW Cirk KW Circ COS Home COS HOME Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory; Human carboxylesterase family member 53010 coding sequence 23-SEP-2002 ABN84302; ABN84302 standard; cDNA; 2158 BP. (first entry)

ALIGNMENTS

diagnosis; gene therapy; gene; ss.

Homo

sapiens

Location/Qualifiers

.1841

product= "53010"
note= "the CDS is also claimed in Claim

27-JUN-2002

WO200250256-A2

mat_peptide

/*tag= ~ 174. 1838 /nocc 96. .173

sig_peptide

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present nucleotide sequence, the coding region of which is also CC claimed, is that of cDNA encoding human 53010, a novel member of the CC carboxylesterase family. The invention provides 53010 nucleic acids, CC antisense molecules, expression vectors, host cells, transgenic animals, CC 53010 proteins, fusion proteins, antigenic peptides, anti-53010 CC antibodies and methods for detecting the presence of 53010 polypeptides CC or nucleic acids, of identifying a compound that binds to the 53010 CC polypeptide, and of modulating the activity of the polypeptide. The 53010 CC polypeptide, and of modulating the activity of the polypeptide. The 53010 CC polypeptide, and polypeptides can act as novel diagnostic and CC therapeutic agents for controlling disorders involving aberrant or CC deficient hydrolysis of carboxylic esters. As 53010 malecules can CC expression is regulated in some rodent pain models, 53010 molecules can also act as novel diagnostic targets and therapeutic agents for CC controlling neurological disorders, such as pain-related disorders. A CC claimed method of tracting or preventing a disorder (especially a pain-cc appressing cell involves administering a compound that modulates 53010 CC expressing cell involves administering a compound that modulates 53010 CC activity or expression. 53010 nucleic acids are also useful in chromosome marays, for detection of variations or mutations, as surrogate markers and control of the control of carrays, for detection of variations or mutations, as surrogate markers
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04-FEB-2003;
27-MAR-2003;
08-MAY-2003;
19-MAY-2003;
16-JUL-2003;
16-JUL-2003;
02-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urological disorder; uropathic; cytostatic; urinary incontinence; benign prostatic hyperplasia; human; gene; ss.
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Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological
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disorder or identifying and treating a subject having a urological disorder.

The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder. Or treating a subject having a urological disorder: Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present

0 Ģ 0 Other;

US-10-023-515-2 (1-581) x ADQ89093 (1-2158)	Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
x ADQ89093	4.71e-282 3079.00 100.00% 100.00% 100.00%
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¥	1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCysPhePheLeuIleLeuGlnPro 20	õ
ъ	96 ATGCCACAGGGACTTACTTCATCTGCTTCACAATGGTGCTTTTTTCCTGATTCTCCAGCCC	155
¥	21 LeuLeuGlyHisArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsn	40
ğ	156 CTGTTGGGACACAGACAGTGGGGGAAAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAAC	215
¥		60
ğ	216 ACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTG	275
¥	61 AsnValPheLeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsn	08
쓩		335
¥		100
岁	336 CCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTAACCCTAATTTGTGC	395
¥	101 LeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLys	120
8		455
¥	121 PheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThr	140
Ъ		515
¥	141 GlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAla :	160
ᅜ		575
Ϋ́	161 SerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGln :	180
ይ		635
¥	181 TyrArgLeuGlyIlePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTrp :	200
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                                              ArgValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAgpMetLeuHis
                                                                                                      ThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluPro
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The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. I activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropineuroprotective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorecti

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KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; Parkinson's disease;
KW wound healing disorders; atherosclerosis; Parkinson's disease;
KW alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW distammation; neoplastic disease; nervous system disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW cone photo- transduction deficiency; neurological disease; stroke;
KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
XX growth abnormality; precocious puberty; gene; ss.
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06-FEB-2001; 2001US-026797P.
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SMITHKLINE BEECHAM
GLAXO GROUP LTD.
                                                                                                                                                                                                                              proteins and polynucleotides useful as vaccines for preventing ing various diseases e.g. cancer, wounds, atherosclerosis, n's disease, Alzheimer's disease, infection, autoimmune disorder
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The invention relates to an isolated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, where the disorders immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis, cirrhosis, hepaticis, and cancer; a neurological disorder such as Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease, a developmental disorder such as reached as relationating to the such as adenoma, thrombosis and infections; an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic disorder such as conjunctivitis, glaucoma, cataract; agastrointestinal
                                                                                                                                                                                                                                 Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal
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15-DEC-2000; 2000US-0256189P.
21-DEC-2000; 2000US-0257713P.
19-JAN-2001; 2001US-0252706P.
02-FEB-2001; 2001US-0266020P.
                                                                                                                                                                                                Claim 78; Page 167-168;
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g J, Walia NK, Nguyen DB, Gandhi
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         gene therapy; human diagnostic
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       and therapeutic polynucleotide;
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Query DB:

Match:

US-10-023-515-2 (1-581) x ACN42766

(1-2229)

Percent Similarity: Best Local Similarity:

6.17e-263 2878.00 99.82% 99.64% 93.47%

Length:
Matches:
Conservative:
Mismatches:
Indels:

Alignment Scores:

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ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu

333 30 70 393 90

ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla

GlyProSerAlaGluGlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGln

274

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The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine CC disorder, neurological disorders, developmental disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence that for this patent is not represented CC in the printed specification, but was obtained in electronic format CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV, Mooney EM, Delegane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gatury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
Sequence
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-329368/30.
P-PSDB; ABM84114.
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               AspAlaGlyAlaProValTyrPheTyrGluPheArgHisArgProGlnCysPheGluAsp
                                                  GACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGA
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유 밁 S

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

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Yamamoto J,
Seki N, Yosh
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P-PSDB; ADB64065.
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25-JAN-2002;
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RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                            f, Sugiyama T,
J, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Claim 1; Page; 222pp; English.
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The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide or peptide of the polynucleotide by contacting the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polynucleotide in an CC expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide or cc is useful as a primer for synthesising the polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide or as a probe CC for detecting are useful as pharmaceutical agents and many disease-related CC genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets CC regeneration. Membrane proteins, signal transduction-related proteins, cancer, tumours The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The Sequence presented is a cDNA of the invention. Note: Some of the sequence CC data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

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Sequence 2092 BP; 464 A; 552 C; 497 G; 579 T; 0 U; 0 Other;

g &	B &	g &	B &	дь Ф	음	B &	B 8	gb Qy	US-10-023-515-2	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:
180 nTyrargLeuGly11ePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTr	160 aSerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGl	140 rGlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAl 	120 sPheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspTh 	100 sLeuglnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLy	84 AlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeu	64 LeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsnProGlnPro	44 GlyTrpileGlnGlyLysGlnValThrValLeuGlySerProValProValAsnValPhe	24 HisargGlnTrpGlyLysThrGlyProSerA	15-2 (1-581) x ADB62095 (1-2092)	tt Scores: 7e-263 Length: 2877.00 Matches: Similarity: 98.40\$ Conservativ al Similarity: 98.04\$ Mismatches: tch: 93.44\$ Indels:
ThrTrpAspGlnHisAlaProGlyAsnTr 200 ACATGGGATCAGCATGCTCCGGGGAACTG 656	TyrGluAspValLeuValValValValG1 180	ProGlyGlyAlaPheLySThrGlySerAl 160 	ASDITETYFALAPFOALAHISALAASDTh 140 	GInHisMetLeuLysValHisTyrProLy 120 CAACACATGCTCAAGGTGCATTACCCGAA 416	ThrSerTyrProAsnLeuCy 100 	31YSerLeuargPheThrAsnDroGlnDro 83 SATCCCTGCGATTTACGAACCCGCAGCCT 296	.euGlySerProvalProvalAsnvalPhe 63 !TGGGAAGCCCTGTGCCTGTGAACGTGTTC 236	<pre>sArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsnThrArgLeu 43 </pre>		1: 2092 38: 551 vative: 2 cches: 2 3: 7

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W Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; (w nootropic; neuroprotective; immunosuppressive; haemostatic; W antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; w wound healing disorders; atherosclerosis; Parkinson's disease; M Alzheimer's disease; autoimmune disorder; haematopoietic disorder; w inflammation; neoplastic disease; nervous system disorder; w inflammation; neoplastic disease; nervous system disorder; w cardiovascular disorders; pancreatitis; respiratory disorder; w hyperproliferation; systemic autoimmune disease; hyper-immunity; w cardiovascular disease; metabolic disease; sperm dysfunction; neuropathy; w haematological disease; metabolic disease; sperm dysfunction; w thyroid disorder; hypothyroidism, brain damage; colitis; w cone photo- transduction deficiency; neurological disease; stroke; w angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; w traches; thymus; lymph node; muscular system; obesity; anorexia; w growth abnormality; precocious puberty; gene; ss.
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09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
   The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootrog
                                                                                                        Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
neuroprotective,
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DB; ABP61005.
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GLAXO GROUP LTD.
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A, Rizvi S
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; 2000US-0257048P.

; 2001US-026048P.

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; 2001US-026797P.

; 2001US-0276988P.

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ValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGlyGlu
                                                                                TrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSarTrp
                                                                                                                                         GAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACA
                                                                                                                                                                      GluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhePheThrThr
                                                                                                                                                                                                                                                       GlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                           HisMetLeuLysValHisTyrDroLysDheGlyValSerGluAspCysLeuTyrLeuAsn 131
                                                        TGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGG
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GTCCAGAAGAACATCGAGTT

IGCTCTGTGACCATCTTTGGCGAG

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                                                                                           CTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGAGAGATGTG 1635
                                                                                                      LeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluProArgValAspPhe
                                                                                                                                   GlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyr
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Yamamoto
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24-JAN-2002;
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o J, Isono Y,
Yoshikawa T,
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Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
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RES ASSOC BIOTECHNOLOGY.
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2002US-0350435P.
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Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                         Ishii S;
R, Tamechika
                           H;
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy. in

Claim 1; SEQ ID NO 736; 205pp; English.

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

428 A; 541 C; 473 G; 520 T; U; 0 Other;

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3.57e-237
2606.00
88.77%
88.25%
84.64%
(1-1962)
                                   Length:
Matches:
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                 Mismatches:
Indels:
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GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAspGln
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                                                                                                                                 AlaGlyAlaProValTyrPheTyrGluPheArgHisArgProGlnCysPheGluAspThr
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                                                                                                                                                                                                                                                                                        AlaAsnGluTyrPheHisAspLysHisSerLeuThrGluIleArgAspSerLeuLeuAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.
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                                                                                                                                                                                                                                   AspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHis 350
                                                                                                                                                                                                                                                                                GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130
         IleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGluPheArgHis 443
                                                                                                                                                                                                      GluCysGlyPheLeuLeuProMetLysGlu-----AlaProGluIleLeuSerGlySer
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                                                                                                              ProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHisSerLeuThr
                                                                                                                                              AACCGTGATGCAGCTTTGGCTTCAACAGCTGGGCATTTCCACAGAAGA-----CATATC 1152
                                                                                                                                                                  AsnLysSerLeuAlaLeu-----
                                                                                                                                                                                        GAGTGTGGCTTCCTGCCTATGGTAAGAATTCTGGCTGTCCATACTGCCACTCCCTCA
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                                                                | YASDValPhePheValValProAlaLeu 423
                                                                                                                                                                   -HisLeulleGlnAsnIleLeuHisIle 383
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06-CCT-2000; 2000US-0238864P.
20-CCT-2000; 2000US-0247381P.
16-NOV-2000; 2000US-0249519P.
22-NOV-2000; 2000US-0252834P.
30-NOV-2000; 2000US-0252834P.
                                                                                Azimzai Y
Elliott V
Lal P, L
Ring HZ,
Walsh RT,
                  WPI; 2002-362498/39
P-PSDB; ADR19663.
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                                                                           ii Y, Baughin MR, B
It VS, Gandhi AR, G
Itee EA, Lu DAM, II
IZ, Sanjanwala MS, Y
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                                                                Borowsky ML, Ding L, Duggan BM;
Griffin JA, Hafalia AJA, Ison CH, KI
Nguyen DB, Arvizu C, Policky JL, R;
Tang YT, Tribouley CM, Narinder WK;
'u Y, Yang J, Yao MG, Yue H;
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Human drug metabolizing enzymes, useful disorders associated with aberrant (DME) autoimmune disorders. l in the diag
E) activity, diagnosis (and treatment cancer and 얁

Claim 12; SEQ ID NO 20; 142pp; English

This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a gene which encodes a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.

Sequence 1857 BP; 428 A; 487 Ç 496 ç, 446 H, 0 U; 0 Other;

δ 닭 δ 밁 5 밁 δ Ś 밁 S 밁 밁 δ 밁 Alignment S Pred. No.: 5 밁 S 밁 Ş US-10-023-515-2 (1-581) x ADR19681 (1-1857) Percent Similarity:
Best Local Similarity:
Query Match:
DB: 211 191 754 694 171 634 574 151 131 514 111 454 394 334 274 91 71 51 31 TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC TyrGluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhePheThr ccaddaddrigeerreaadaeredereadeerecarerraareddreedeececedeerece ProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAla AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe GlnHisMetLeuLysValHisTyrProLysDheGlyValSerGluAspCysLeuTyrLeu 130 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC CAACATATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG CGAGAAGCCACCTCCTAACCCTAATTTGTGCCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 513 dreactdracidadaadecerbracerdaaacdrarecerdaadrececertracerder ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla 70 ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu 90 GlyProSerAlaGluGlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGln 1.52e-235 2588.50 94.62% 94.42% 84.07% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1857 491 12351 230 813 210 190 693 170 150 753 633 573 453 393 50

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RESULT 11
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ID ADF50
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Novel cauxin protein or its salt, useful
                                                                                                                                                                                      cat; cauxin; cat kidney disease marker; kidney disease; gene;
                                                                                                                     WPI; 2004-002277/01.
                                                                                                                                        04-MAR-2002;
                                                                                                                                                 04-MAR-2002; 2002JP-00057908
                                                                                                                                                           09-SEP-2003
                                                                                                                                                                    JP2003250575-A.
                                                                                                                              (TOHO-) TOHOKU TECHNOARCH KK
                                                                                                                                        2002JP-00057908
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                                                                                                       cat
                                                                                                       kidney
                                                                                                       disease
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diagnosing cat kidney disease.

Claim 6; SEQ ID NO 3; 33pp; Japanese.

The present sequence encodes a cat cauxin protein (I) or its salt, which CC is cat kidney disease marker. Also described: (I) a partial peptide (II) CC of (I); (2) a nucleic acid (II) encoding (I) or (II); (3) a vector (IV) CC comprising (III); (4) a transformed host (V) comprising (III) or (IV); (C comprising (III); (1) a transformed host (V) comprising (III) or (IV); (C comprising (I) or (II) by culturing (V); (6) a antibody (VI) which CC couples specifically with (I) or (II); (7) diagnosing cat kidney disease CC which involves measuring (I) quantitatively, and where reduction of CC amount of (I) indicates presence of the disease; (8) a cat kidney disease CC diagnostic agent comprising (I) labelling agent, a reagent which measures CC the biological activity of urinary (I) or (VI); and (9) a cauxin CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney CC disease marker semant which measures simple. (I) is useful as a CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, blood testing.

Sequence 2145 BP; 444 A; 581 C; 550 G; 564 T; 0 U; 6 Other;

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Best Local Similarity:
Query Match:
DB:
                       Percent Similarity:
                               Score:
                                              Alignment Scores:
                                       Мо.:
5.74e-181
2015.00
80.87%
70.04%
65.44%
                       Length:
Matches:
Conservative:
        Mismatches:
Indels:
2145
388
60
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US-10-023-515-2 (1-581) x ADF50146 (1-2145)

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                                         GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130
AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe 150
                                                                         CGAAATGCCACATCCTACCCTAAATTATGCTTCCAGGACTTAGAGTGGCTGGTCTCCTAT 477
                                                                                      CCTCCTCTAGGGCCCCTGCGATTTAAGCAACCAAAGCCTGCTCTGCCCGGGAATGACTTC
                                                                                                                                       ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu
                         CAACACGTTCTCAAAGTGCGTTACCCCAAATTGGAAGCGTCCGAAGACTGCCTGTACCTT
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Cat cauxin encoding cDNA SEQ ID NO:3.

12-FEB-2004 ADF50146;

(first entry)

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LeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGly
                                                                       GlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThxGluGluGluLysLeu
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Percent Similarity:

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Length: Matches: Conservative:

Pred. No.: Alignment Scores:

Sequence 1629

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ABQ86171;

Novel human gene. (first entry) SEQ ID 42.

KW Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; KW mootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; kW wound healing disorders; atherosclerosis; Parkinson's disease; kAlzheimer's disease; autoimmune disorder; haematopoietic disorder; kM hlzheimer's disease; autoimmune disorder; haematopoietic disorder; kW niflammation; neoplastic disease; nervous system disorder; kW hyperproliferation; systemmic autoimmune disease; hyper-immunity; kW hyperproliferation; systemmic autoimmune disease; hyper-immunity; kW hyperproliferation; systemmic autoimmune disease; hyper-immunity; kW heematological disease; metabolic disease; sperm dysfunction; heematological disease; metabolic disease; sperm dysfunction; kW thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; kW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; kW trachea; thymus; lymph node; muscular system; obesity; anorexia; kW growth abnormality; precocious puberty; gene; ss.

sapiens.

WO200250105-A1

17-DEC-2001; 2001WO-US049232.

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30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
08-MAY-2001;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a polypeptide-human carboxylatase-24.64, the polymucleotide for coding it, the process for preparing the polypeptide by DNA recombination, the application of the polypeptide in treating diseases such as primary hypertension, digestive ulcer, nephrotic, bronchial asthma, tremor, etc, the antagon of the polypeptide and its medical action, and the application of the polynucleotide are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1244
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                       New peptides and its encoding nucleic acid derived from intestinal carboxyesterase, useful as immunostimulants for treating cancer.
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US-10-023-515-2 (1-581) x AAF25258 (1-1680)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1680 BP; 345 A; 475 C; 488 G; 372 T; 0 U; 0 Other;
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                    MetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleDroTyr
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ATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGAGTGGCGTGGCCTCCTGCCCGGC
                                                                                                             ValThrIlePheGlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerPro
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CACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCC
                         ProArgValAspPheTrpThrSerThrIlePro 550
                                                   CAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGGGCCGGGCTCTGAAGGCC
                                                                     LeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu
                                                                                                                             ThrPheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsn
                                                                                                                                                               TTC-----ACTGAGGAAGAGGAGCAGCTAAGCAGGAAGATGATGAAGTACTGGGCC
                                                                                                                                                                                 PheGluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAla 499
                                                                                                                                                                                                                                                                                                                                                     ValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyr
                                                                                                           AACTTTGCGAGAAATGGGAACCCCAATGGCGAGGGTCTGCCCACACTGGCCGCTGTTCGAC
                                                                                                                                                                                                                 HisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMet 479
                                                                                                                                                                                                                                                                            GAGTTCCAGCATCAGCCCAGCTGGCTCAAGAACATCAGGCCACCGCACATGAAGGCAGAC
                                                                                                                                                                                                                                                                                                     GluPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAsp
                                                                                                                                                                                                                                                                                                                                 ATCCCTGCACTCCAAGTAGCACATTTT---CAGTGTTCCCGGGCCCCTGTGTACTTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluAlaProGluIleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsn
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Search completed: June Job time : 910 secs 15,

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-fgn2 1/USPTO_spool/664091/runat 14062005 133643 10569/app_query.fasta_1.775
-DB=PublIshed_Applications_NA -QFMT=Fastap_SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END==1 -MATRIX=bibosum62
-TRANS=human40.cdi -LIST=45 -DCALIGN=200 -THR SCORE=pct -THR MXX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=6664091 @CGN 1 1 480 @runat 14062005 133643 10569
-NCPU=6 -ICPU=3 -NO MANA -LARGEOUTERY -NEGS-SCORES=0 -WAIT_DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=10 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have

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SUMMARIES

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RESULT 2
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Sequence 3, Application US/10674636
; Publication No. US20040086922A1
; GENERAL IMFORMATION:
; APPLICANT: CUITIS, ROTY A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN
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 HUMAN CARBOXYLESTERASE
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Sequence 1, Application US/10023515

Publication No. US20020182636A1

GENERAL INFORMATION:
APPLICANT: CURLES, ROTY A. J.
APPLICANT: SILOS-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2158
TYPE: DNA
ORGANIGM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (96)...(1838)
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                                                                                             GAAGGAGCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACC 1595
                                                                                                           GluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThr
                                                                                                                                                          AlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPhe 480
                                             TTTGCTCGAACCGGAATCCTAATGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTG
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\$ \$ \$ \$ \$ \$ \$	QQ QQ	B Q B Q	3 8 8 8	B & B &	D Q D Q	D Q D	8 8 8 8 8 8
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APPLICANT: KAICHELI, Venkateswarlu

APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: Silos-Santiago, Inmaculada

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APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: MCDICAGICAL DISORDERE USING 44390, 54161, 211, 5687, 884,

TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18500, 2047,

TITLE OF INVENTION: 130751, 52872, 14063, 20739, 32544, 43329, 4373, 51164,

TITLE OF INVENTION: 130751, 52872, 15985, 15285, 760, 18603, 2395, 2554, 8675,

TITLE OF INVENTION: 23720, 4899, 14303, 16616, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 23720, 4899, 14303, 16616, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2359, 8863, 1402, 16209, 16386, 21155, 30911, 44897, 1643,

TITLE OF INVENTION: 2505

TITLE OF INVENTION: 2505

TITLE OF INVENTION: 2505

TITLE OF INVENTION: 25043, 9826, 13231, 32409, 84260, 2882, 8203, 32678 OR

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 577, 619, 1423,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2505-01, 16816, 17827, 32620, 30911, 44897, 1643,

TITLE OF INVENTION: 2500-01, 16816, 17827, 32620, 30911, 44897, 1643
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US-10-757-262-45
                      LENGTH: 2158
TYPE: DNA
ORGANISM: Homo
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; LOCATION: (96).
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Best Local Similarity:
Query Match:
DB:
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RESULT 6
US-10-451-168-40
US-10-451-168-40
; Sequence 40, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.1.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
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; TYPE: DNA
; ORGANISM: Homo s
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PRIOR APPLICATION NUMBER: PCT/USO1/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-20
PRIOR PRILING DATE: 2001-01-20
PRIOR PRILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-02-06
PRIOR PRILING DATE: 2001-03-09
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PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281, 535
PRIOR PILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289, 622
PRIOR FILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
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PRIOR FILLING DATE: 2001-01-30
PRIOR PELICATION NUMBER: 60/266,797
PRIOR FILLING DATE: 2001-02-06
PRIOR PELICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILLING DATE: 2001-04-04
PRIOR FILLING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILLING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4
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                IleLeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuSerLeu
                                                                                                SerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThr1leProLeu 551
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APPLICANT: AVIZOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: ARVIZO, Chandra S.; RING, Huijun Z.
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: YUE, Henry; TRIBOULEY, Catherine M.
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
APPLICANT: U, Dyung Aina M.; LAL, Preeti G.
APPLICANT: CHAWLA, Narinder K.; VANG, Junming
APPLICANT: GANDHI, Ameena R.; LU, Yan
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                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
         US-10-023-515-2
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PRIOR APPLICATION NUMBER: PCT/US01/49232

PRIOR FILING DATE: 2000-12-17

PRIOR PRIOR PAPELICATION NUMBER: 60/256,710

PRIOR PRIOR DATE: 2000-12-19

PRIOR PPLICATION NUMBER: 60/257,048

PRIOR PILING DATE: 2000-12-20

PRIOR PILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/264,922

PRIOR FILING DATE: 2001-01-09

PRIOR PPLICATION NUMBER: 60/266,797

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR PILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: 60/276,988

PRIOR PILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/281,535

PRIOR APPLICATION NUMBER: 60/281,535

PRIOR PILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/281,535

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SEQ ID NO 41
LENGTH: 1746
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                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. APPLICANT: GLAXO GROUP LIMITED
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                                                                                                                                                               LysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAsp
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US-10-094-749-736
; Sequence 736, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
     APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHI, SHIZUKO
APPLICANT: ISHI, SHIZUKO
APPLICANT: ISHO, YUUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: HISONO, YUUKO
APPLICANT: HISONO, YUUKO
APPLICANT: OTSUKA, KAORU
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: WAGHARI, KENUI
APPLICANT: WAGHARI, KENUI
APPLICANT: WAGHARI, KENUI
APPLICANT: WAGHARI, KENUI
APPLICANT: WAGHARI, KENUI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILLE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CUERCENT ETLING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER: DETATION UNDER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER: DETATION UNDER: JP 2001-328381
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Percent Similarity:
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Query Match:
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Sequence 195, Application US/10114270
Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kokuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Liu, Ziaohong
APPLICANT: Guev, Vladimir Y.
APPLICANT: Li, Li
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US-10-114-270-195
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PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR PLING DATE: 2001-04-17
Remaining Prior Application data removed - See
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 195
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KBY: CDS
LOCATION: (1)...(1744)
US-10-114-270-195
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Shenoy, Suresh G.
Pena, Carol B.A.
Smithson, Glennda
Burgess, Catherine B.
Gerlach, Valerie
ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla 70
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APPLICANT: MALMANI, TALLA, DING, LI;
APPLICANT: BOROWSKY, Mark L.; DING, LI;
APPLICANT: BOROWSKY, Mark L.; DING, LI;
APPLICANT: GANDHI, Amena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, FARTAN A.; LAL, Preeti G.;
APPLICANT: KHAN, FARTAN A.; LAL, Preeti G.;
APPLICANT: RAWKUMAR, J., LAL, Preeti G.;
APPLICANT: RAWKUMAR, J., LAL, Preeti G.;
APPLICANT: RAWKUMAR, J., PRING, Huijun Z.;
APPLICANT: SANJANWALA, Madhusudan M.;
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
FILE REFERENCE: PI-023 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR APPLICATION NUMBER: US 60/252,834
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PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-30
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PRIOR FILING DATE: 2000-11-30
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Publication No. US20040086887A1

GENERAL INFORMATION:

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APPLICANT: BOROWSKY, Mark L.; DING, Li;

APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;

APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;

APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;

APPLICANT: KHAN, Farrah A.; Li, Dyung Aina M.

APPLICANT: KHAN, Farrah A.; LU, Dyung Aina M.

APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennife.

APPLICANT: RAWKUMAR, Jayalaxmi, RING, Huijun Z.

APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.

APPLICANT: CHANGLA, Marinder K.; WALSH, Roderick

ADDITCANT: CHANGLA, Narinder K.; WALSH, Roderick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-381-898-20
                                                     NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 1857
TYPE: DNA
ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
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US-10-381-898-20
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APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG PP02US006
CURRENT FILING DATE: 2002-09-03
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2145
TYPE: DNA
ORGANISM: Felis catus
PEATURE:
NAME/KEY: CDS
LOCATION: (175)..(1803)
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OTHER INFORMATION: n is a,
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|TACGAGGACGTGCTGATCGTGACTACCCAGTACCGGCTAGGAATATTTGGTTTTTTTCGAC
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Sequence 1, Application US/1023393A

; Sequence 1, Application US20040214171A1

; GENERAL INFORMATION:

; APPLICANT: Yamashita, Tetsuro

; APPLICANT: Miyazaki, Masao

; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER

; FILE REFERENCE: SHIG FP02US006

; CURRENT PILING DATE: 2002-09-03

; CURRENT FILING DATE: 2002-09-03

; PRIOR APPLICATION NUMBER: US/10/233,933A

; CURRENT FILING DATE: 2002-04-03

; PRIOR FILING DATE: 2002-04-03

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1629

TYPE: DNA

; ORGANISM: Felis Catus
              Alignment Scores: Pred. No.:
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                                                                                                                                     GACTOTGCTGCTGCTGCAGTGCCTGAGGGCAAAAACCCTCCGAGGAGTTGATGGACATC
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                            GTAGCCCTATTGACTCAAAAAGCATTTAATTCAGTTCCTTCTATCATCGGAGTCAATAAC
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Mismatches:
Indels:
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903 309 843

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663 230 603 210 543

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FILE REFERENCES: GP50039

CURRENT FILING DATE: 2003-11-12

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: GCT/US01/49232

PRIOR FILING DATE: 2000-12-17

PRIOR FILING DATE: 2000-12-17

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR PILING DATE: 2000-12-20

PRIOR PILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/264,922

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-03-19

PRIOR PILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/281,535

PRIOR PILING DATE: 2001-04-04

PRIOR APPLICATION NUMBER: 60/299,622

PRIOR PILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 110

SOPTWARE: FASE(SEQ for Windows Version 4.0

SEQ ID NO 42

LENGTH: 1071
                                                                                                                                                                                                                                                                                                                                                                                            US-10-451-168-42

S-10-451-168-42

; Sequence 42, Application US/10451168

; Publication No. US20040091969A1

; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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         GlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPhe
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                                                           AlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeuThr
                                                                                                                                                                               AspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGlu
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Search Job ti	д	ş	DЬ	ş
Search completed: June 15, 2005, 15:44:59 Job time : 994 secs	1009 CCTCTTTCCTTCCCTCTCTCTCTCCCTCCAGCCTTTCTTT	562 ProLeuSerSerLeuThrPheLeuSerLeuLeuGlnProPhePhePhePhePheCysAlaPro 581	949 GTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGT 1008	542 ValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAspMetLeuHisSer 561

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
6: geneseqp203as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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3079
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ન	_U	4.	w	N	H	NO.	Result
1186.5	1191	1213.5	1221	1230	1230	1230	1230	1230	1230	1230	1262.5	1780	1985	1985	2454	2588.5	2597.5	2606	2607.5	2900	2900	2915	3079	3079	Score	
38.5	38.7	39.4	39.7		39.9	39.9		39.9	39.9	39.9	41.0	57.8	64.5	64.5	79.7	84.1	84.4	84.6	84.7		94.2	•	100.0	100.0	Match I	Query
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Adi79890 Mouse liv	Abu53222 Human met	Add46519 Rat Prote	Human	Add46521 Human Pro	Aae33960 Human car	Abb82851 CES2 rela	Humai	Aab31700 Protein e	Adg98219 Human int	Aab58981 Breast an	Aae20911 Rat carbo	Abp61006 Novel hum	Adf50147 Cat cauxi	Cat ca	Adb64065 Human pro	Adr19663 Human dru	Abu54639 Human NOV	Ada54807 Human pro	Abp61005 Novel hum	Abm84114 Human dia	Human	Abp61004 Novel hum	Adq89094 Human uro	uman c	Description	

53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases; as surrogate markers, in tissue typing and chromosome mapping.

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	
1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	
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Abu81549	Abu67116	Abu82152	Abo25111	Abu69085	Abu59921	Abu66840	Abo19424	Abu81140	Abo33809	Abu80843	Abu69108	Abo17886	Abg64341	Abb84949	Aau83696	Aae04101	Aau12442	Aay71107	
Human	Human	Novel	Human	Human	Novel	Human	Human	Human	Novel	Human	Human	Novel	Human	Human	Human	Human	Human	Human	
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ALIGNMENTS

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28-MAR-2001;
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                                                                                                                                                    WPI; 2002-547936/58.
N-PSDB; ABN84302.
                                                                                                                                                                                                                                             Curtis RAJ,
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2001US-0279508P
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Matches 581
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CC cespecially a pain-related disorder) characterised by abstrant activity of a $3010 expressing cell involves administering a compound that
CC modulates $3010 activity or expression
    ADQ89094;
                              ADQ89094 standard;
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                                                                                                                     RVDEWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP 581
                                                                                                                                                                                 EGATEBEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNWSLGQRLKBP
                                                                                                                                                                    EGATEEEKLLSRKMMKYWATFARTGNPNGNDI
                                                                                                                                                                                                                        PALITAR YHRDAGA PVYFYEFRHR POCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                           PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                                                                     APRILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTRIRDSLLDLLGDVFFVV
                                                                                                                                                                                                                                                                                                       APEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVV
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                                                                                                                                                                                                                                                                                                                                                KPSKELLTLSQKTKSFTRVVDGAFFÞNEPLDLLSQKAFKAÍÞSÍÍGVNNHECGFLLÞMKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRLGIFGFFTTWDQHAFGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGVSEDCLYLNIYAPAHADIGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGVSEDCLYLNÍYAÞÁHAÐTGSKLÞVLVWFÞGGAFKTGSASIFDGSÁLAAYEÐVLVVVVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHNLKVHYPK
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                              protein;
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                                                                                                                                                                                                                                    The present invention describes the use of polypeptides related to C urological disorders for identifying a compound capable of treating a C urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a CC method for identifying a compound capable of treating a urological CC disorder; (2) a method for identifying a subject having a urological CC disorder; and (3) a method for treating a subject having a urological CC disorder; The compound has uropathic and cytostatic activities. The CC polypeptides related to urological disorders are useful for identifying a CC compound capable of treating a urological disorder, identifying a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic disorder. Disorders include urinary incontinence and benign prostatic charing aurological disorder related protein, which is used in the exemplification of the present cc invention.
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Best Local
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18-JUL-2003;
30-JUL-2003;
02-SEP-2003;
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04-FEB-2003;
27-MAR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM
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19-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urological disorder; uropathic; cytostatic; urinary incontinence;
benign prostatic hyperplasia; human.
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                                                                                                                     1 MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; SEQ ID NO 46;
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                                                                                                                                                                                    Similarity
FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQ
                                             NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPK
                                                                  NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPK 120
                                                                                                      MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
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2003US-0468775P
2003US-0471614P
2003US-0478742P
2003US-0488529P
2003US-0499156P
2003US-0499594P
2003US-0499594P
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2003US-0444783P.
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Pred. No. 1e-278;
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19-DEC-2000;
20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
                                                                                                                                                                                                                                              wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyper-immunity; gustemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy. haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart traches; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP61004 standard; protein;
                                                                                                                    17-DEC-2001;
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2000US-0256710P.
2000US-0257048P.
2001US-0260482P.
2001US-0264922P.
2001US-0264922P.
2001US-026797P.
2001US-0276988P.
2001US-0281535P.
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                                                                                                                    2001WO-US049232
                                                                                                                                                                                                                                     precocious puberty
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The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC extostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, notropic, curotatic, vulnerary, antiarteriosclerotic, antiparkinsonian, notropic, cardiant, antilicer, virucide, antityroid, cerebroprotective, anorectic, CC end metabolic. Polypeptides and polynucleotides of the invention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and CC hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, cancers etc. Alzenderoscial diseases, metabolic diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone phototransduction deficiency, neurological diseases, stroke, angiogenesis, CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart, CC transduction deficiency, neurological diseases, stroke, angiogenesis, CC ovulation disorders, and alleviation of precocious puberty. The CC growth abnormalities, and alleviation of precocious puberty. The cc growth abnormalities, and alleviation of precocious puberty. The cc growth abnormality in records ABP60965-ABP61019 represent novel human
  Best Local Sim Matches 553;
                                       Query Match
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(SMIK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                 Sequence 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1(a); Page 312-313; 335pp; English.
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7 SA,
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SMITHKLINE BEECHAM
GLAXO GROUP LTD.
                       Similarity
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A, Rizvi SK,
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97.0%;
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Smith RF, Strum JC,
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Score 2915; DB 5;
Pred. No. 2.3e-263;
3; Mismatches 6;
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LALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRD
                                      KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
                                                                                                       HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ
                                                                                                                                                        WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                                                                                                                                                                           IYAPAHADIGSKLPVLVWFPGGAFKTGSASIFPDGSALAAYEDVLVVVVQYRLGIFGFFTT 191
                                                                                                                                                                                                                                              PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN
                                                                                                                                                                                                                                                         PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN 131
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                                                                                        HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ
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   Sanjanwala MM, Yao
Lee EA, Ding L, H
Lal PG, Warren BA,
                                                                        08-DEC-2000; 2000US-0254308P.
15-DEC-2000; 2000US-0256189P.
21-DEC-2000; 2000US-0257713P.
19-JAN-2001; 2001US-0252796P.
02-FEB-2001; 2001US-0266020P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis; proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; Huntington's denoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer; anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10.
                                                                                                                                                   04-DEC-2001; 2001WO-US047429.
                                                                                                                                                                                                                                                                                        Domain
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Yao MG, Au-Young J, Bau
L, Hafalia AJA, Tang YT,
a BA, Yang J, Walia NK,
                                                    GENOMICS
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/label= Signal_peptide
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  Baughn MR, Ar
YT, Yue H, Tr
NK, Nguyen DB,
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DB 5;

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CC are selected from autoinmune/inflammatory disorder such as acquired curvatures, such as acquired conventis; a cell proliferative disorder such as arteriosclerosis, psoriasis, coll proliferative disorder such as arteriosclerosis, psoriasis, collectives, hepatitis, and cancer; a neurological disorder such as acteriosclerosis, and cancer; a neurological disorder such as collectives, and cancer; a neurological disorder such as collectives, epilepsy, collectives, and cancer; a neurological disorder such as conjunctivitis, glaucoma, parkinson's disease; collectives, and evelopmental disorder such as adenoma, thrombosis and infections collectives, and eye disorder such as conjunctivitis, glaucoma, cataract; metabolic collectives, and eye disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal collectives as anoraxia, peptic ulcer; and liver disorders. DME is consolid to a number of drug screening techniques and to analyse the consolid collective or cell type. The invention is useful for creating collective in somatic or germline gene therapy, to generate a transcript image of a classue or cell type, for detecting differences in the chromosomal collective discorders in the chromosomal collective discorders in the chromosomal collective discorders, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10
  Sequence 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated human drug metabolising enand its nucleotide. DME is useful for diagnosing, treating or published associated with aberrant expression of DME, where the are selected from a trivial discreases are selected from the contraction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal
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N-PSDB; AAD40574.
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Ś 멼 Ş 문 Ś 밁 S 밁 S 밁 Ś 밁 Ş 밁 8 밁 Ś Matches Query Match Best Local : 451 452 391 392 331 332 271 272 151 548; 31 GPSAEGPORNTRIGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL 92 DLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS Similarity TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGN VANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYBFRHRPQCFED DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEVLSGSNKSLALHLIQNILHIPPQYLHL DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL 330 WVQKNIEFFGGDPSSYTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD 270 REATSYPNICLONSEWILLIDOHMIKVHYPKFGVSEDCIYLNIYAPAHADTGSKLPVLVWF REATSYPNICLQNSEWILLIDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF 150 YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS PGGAFKTGSASIFDGSALAAYEDVLVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS 210 GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL Conservative 94.2%; 2 Score 2900; DB 5 Pred. No. 7e-262; Mismatches Length Indels 0 Gaps 570 510 450 451 391 331 211 151

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JX6XFXBXBX9X9X9X6XFXFXFXF15F15F2FXFXFFFX8X50505050505050505050
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                                                CC The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, condition for the proliferative disorders, conditions caused by virus, bacteria, fungion parasite. The dithp CC disorder, neurological disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungion parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC polymorphisms, as molecular weight maxiers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the CC invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV, Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtor Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gj Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-2004 (first entry)
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Sequence
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12-SEP-2002;
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DB; ACN42766.
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2002US-0410260P.
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                                    www.wipo.int/pct/en/sequences/listing.htm
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Query Match Best Local Similarity

94.2%;

Score Pred.

2900; DB 8; No. 7e-262;

Length 642,

WO200250105-A1 Homo sapiens.

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Matches
                                                                                                                                              nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiinfler; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; wound healing disorders; atherosclerosts; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; haematological disease; bypothyroiddism; brain damage; colitis;
                                                                        cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; hear traches; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty.
                                                                                                                                                                                                                                                                                                                                                                 Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REATSYPNICLONSEWILLIDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The creativity of polypeptides of the invention may be described as, related to vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, cardiant, antilicer, virucide, antithyroid, cerebroprotective, amorectic, cand metabolic. Polypeptides and polynucleotides of the invention are compared to the control of cancer, considered to the control of cancer, considered to the control of cancer, considered to the control of cancer, confidential and the control of cancer, confidential and control of cancer, confidential and control of cancer, confidential and control of cancer, confidential and control of cancer, confidential and control of cancer, confidential and cancer, pancreatitis, respiratory disorder, confidential and disorders, pancreatitis, respiratory disorders, confidential diseases, metabolic diseases, hyper-immunity, confidential diseases, metabolic diseases, sperm dysfunction, thyroid confidential diseases, metabolic diseases, sperm dysfunction, thyroid convolution deficiency, neurological diseases, sperm dysfunction, thyroid convolution disorders, diseases in the spinal cord, thyroid gland, heart, convolution disorders, diseases in the spinal cord, thyroid gland, heart, confidential and control of parecocious puberty. The sequences given in records ABP60965-ABP61019 represent novel human control of the invention
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2000; 2000US-0256710P.
20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0264922P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266979P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0281535P.
08-MAY-2001; 2001US-0289622P.
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Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1(a); Page 313-314; 335pp; English.
WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSYTIFGESAGAISVSSLILSPMAKGLF
                                                                     IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT
                                                                                                                 PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN
                                                                                                                                    PLGSLRETNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN
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SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
                                                IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT
                                                                                                                                                                                          WAIWVLAAP-
                                                                                                                                                                                                 WCFFLILOPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
                                                                                                                                                                                                                                                                                                                        581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins and polynucleotides useful as vaccines for preventing ing various diseases e.g. cancer, wounds, atherosclerosis, n's disease, Alzheimer's disease, infection, autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SA,
                                                                                                                                                                                                                                                     84.7%; ilarity 91.4%; Conservative
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                                                                                                                                                                                ----TKGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
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Pred. No. 1.4e-234;
7; Mismatches 25;
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, Strum JC,
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RESULT 7
ADA54807
ID ADA54807
XX ADA5
AC ADA5
XX ADA5
XX Cytc
CKW Gene
KW infl
XX ING
PD 19-N
XX 14-E
PR 21-N
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                                                                                                                                                                                  New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                         Seki N,
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Yamamoto J,
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24-JAN-2002; 2002US-0350435P.
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RES ASSOC BIOTECHNOLOGY.
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J, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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The present invention relates to novel human secretory or memby proteins (ADA54072-ADA55710) and their coding sequences (ADA524ADA554071). The coding sequences are useful in the gene therapy diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

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Claim 14; SEQ ID NO 2375; 205pp; English.

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Matches
                                                                                                                                                                     Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; acrtic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease; cancer.
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Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhus, Gorman L, Shenoy G, Pena CEA, Smithson G, Burgess CE, (Sportan L, Shenoy B, Pana CEA, Taupier RJ, Casman Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Mazur A, Millet I, Peyman Magdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman Magdougall JR, Magdougall Magdougall Magdougall Me, Mazur A, Millet Magdougall Me, Magd × Spytek KA; et CAM, Zerhusen BD; Casman SJ, Peyman JA;

N-PSDB; 2003-046858/04. ABX72267.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim ۲, Page 303; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polypucleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABU54542-ABU54647 represent human NOVX polypeptides of the invention

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20-OCT-2000;
09-NOV-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                                                                              drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; endocrine disorder; eye disorder; gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
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; 2000US-0238864P.
; 2000US-0242323P.
; 2000US-0247581P.
; 2000US-0249519P.
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Bliott VS, Gandhi AR, Gj
Lal P, Lee BA, Lu DAM, N
Ring HZ, Sanjanwala MS, T
Walsh RT, Warren BA, Xu Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                          VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED
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Griffin JA, Hafalia AJA, Ison CH,
Nguyen DB, Arvizu C, Policky JL,
Tang YT, Tribouley CM, Narinder 1
1 Y, Yang J, Yao MG, Yue H;
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J.6e-233;
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                                                                                     The invention discloses a polymucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polymucleotide CC or ite partial peptide, an antibody binding to the polypeptide or peptide CC of the polymucleotide, immunologically assaying the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polymucleotide in an CC is useful as a primer for synthesising the polymucleotide. The oligonucleotide CC is useful as a primer for synthesising the polymucleotide, or as a probe CC for detecting the polymucleotide. The polymucleotide and encoded genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets CC genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets CC respensation. Membrane proteins, signal transduction-related proteins, concertively or expression of the concertive proteins and genes are involved in tissue and/or cell CC respensation to the used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the invention. Note: Some of the sequence data for this patent is not represented in the printed consecutions and sequence information supplied by the specification, but is based on sequence information supplied by the consecutions of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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25-JAN-2002;
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DB; ADB62095.
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RES ASSOC BIOTECHNOLOGY.
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2002US-00350978.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Sequence 469 AA;

The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector

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Best Local S
Matches 467
                                                                                                                                                Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cat cauxin protein SEQ ID NO:2.
                                                                                                   Claim 3;
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                                                                                                ID NO 2; 33pp; Japanese.
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Pred. No. 2.4e-220;
2; Mismatches 0;
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                                                                                                                                                                                   cat kidney disease marker,
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RESULT 12
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Best Local Similarity
Matches 373; Conserv
                                 JP2003250575-A
                                                                                                                                                                                                                                            12-FEB-2004
                                                                                                                                                                                                                                                                                                 ADF50147;
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                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGVPLWPAYTQSEQYLKLDLSVSVGQKLKEQEVEFWMNTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFENEP 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGGAFKMGSASSFDGSALAAYEDVLIVTTQYRLGIFGFFDTGDEHARGNWALLDQVAALT
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                                                                                                                                 marker;
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CC The present sequence represents a cat cauxin protein (I) or its salt, CC which is cat kidney disease marker. Also described: (I) a partial peptide CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector CC (IV); (5) producing (II) or (II) by culturing (V); (6) a antibody (VI) CC which couples specifically with (I) or (II); (7) diagnosing cat kidney CC disease which involves measuring (I) quantitatively, and where reduction CC of amount of (I) indicates presence of the disease; (8) a cat kidney CC disease diagnostic agent comprising (I) labelling agent, a reagent which CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin CC detection kit which measures cauxin in a test sample. (I) is useful as a CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney CC disease. (I) enables detection of cat kidney disease simply and CC correctly. (I) provides an early marker for the disease, and replaces CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, CC blood testing.
                                 blood testing.
Sequence 542
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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Query Match
64.5%; Score 1985; DB 8; Length 542;
Best Local Similarity 71.7%; Pred. No. 2.4e-176;
Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2

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                                                                                                REATSYPNICLQNSEWILLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
DTRPAFVKADHSDEIRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMRYWANFARTGDPNG
             DTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNG 509
                                                               LVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFE
                                                                                                                                                                                                                   WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYL-EAH
                                                                                                                                                                                                                                                                  PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                 LVADHYFYNKHSPVBIRDSFLDLLGDVLFVVPGVVTARYHRDAGAPVYFYBFQHPPQCLN
                                                                                                                                                    GDÉRKKDLQVLARICGCHASDSAALLQCLRAKPSEELMDISKKLTFSIPVIDDFFFFDEP
                                                                                                                                                                     DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEP
                                                                                                                                                                                                     WVRDNIEFFGGDPRSVTIFGESAGAISVSSLILSPIANGLFHKAIMESGVAILPLLMRPP
                                                                                                                                                                                                                                                    PGGAFKMGSASSFDGSALAAYEDVLIVTTQYRLGIFGFFDTGDEHARGNWALLDQVAALT
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EGVPLWPAYTQSEQYLKLDLSVSVGQKLKEQEVEFWMNTI 540

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RESULT 13
ABP61006
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KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW drifinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; parkinson's disease;
KW drifinemer's disease; autoimmune disorder; haematopoietic disorder;
KW inflammation; neoplastic disease; nervous system disorder;
KW drifinemation; neoplastic disease; nervous system disorder;
KW drifinemation; systemic autoimmune disease; hyper-immunity;
KW drifinemation; systemic autoimmune disease; hyper-immunity;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW haematological disease; metabolic disease; sperm dysfunction;
KW haematological disease; metabolic disease; sperm dysfunction;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW cone photo- transduction deficiency; neurological disease; stroke;
angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2000;
20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, heemostatic, antiinflammatory, cardiant, antiuleer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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Martensen (
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                                                                                                                                                                                                                                                                                                                                                                Claim 1(a); Page 315;
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(GLAX )
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DB; ABQ86171.
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2001US-0264922P.
2001US-026697PP.
2001US-0276988P.
2001US-0276988P.
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A, Rizvi SK,
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                                                                                                                                                                                                                                                    osteopathic; gene therapy; osteoporosis; detoxifying agent; Paget's disease; bone
                                                                                                                                                                                                                                                                                                                                                                                   AAE20911;
                                              (FARB )
                                                                            17-JUL-2000; 2000US-0218564P
                                                                                                         10-JUL-2001; 2001WO-EP007919.
                                                                                                                                            24-JAN-2002.
                                                                                                                                                                        WO200206454-A2
                                                                                                                                                                                                        Rattus
                                                                                                                                                                                                                                       dental
                                                                                                                                                                                                                                                                                                                   Rat carboxylesterase-like enzyme protein.
                                                                                                                                                                                                                                                                                                                                                    01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 AAE20911 standard; protein; 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 356 AA;
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                                                                                                                                                                                                                                                                                     carboxylesterase-like enzyme; organophosphorus intoxication;
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                                               BAYER AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEA 361
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                                                                                                                                                                                                                                       enzyme; gene expression.
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100.0%; Pred. No. 2e-157;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                      antisense therapy; cytostatic;
implant degradation; cancer;
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cc carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is consistent of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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Best Local :
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                                                                                                                             VFGGAFLKGDIVMFEGATEBEKLLSRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQ 526
                                                                                                                                                                                     IQYTEMMGDFLFVIPALQVAHFQR-SHAPVYFYEFQHAPSYFKNVRPPHVKADHADEVPF
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                                                                                                                                                                                                                                         DSLLDLLGDVFFVVPALITARYHRDAGAPVYFYBFRHRPQCFBDTKPAFVKADHADEVRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPRNQLHSWLNAVLFGLLL--LLIHVQ-GQDSPES-SPIRTTHTGQVQGKLDHVKDTKAG
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Pred. No. 1.1e-108;
7; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL

Matches 248; Query Match

Local

Similarity

39.9%;

Conservative

91;

Score 1230; DB 3; Pred. No. 1.2e-105; 1; Mismatches 168;

Length 549; Indels

24;

Gaps

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                                                                            Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nontropic; entrinfilammatory; antivical; antiallergic; hepatotropic; antidiabetic; cc antifilingal; antiparastic and cardiant activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly protein, sequences are used in the diagnosis, prevention and treatment cf immune disorders e.g. Addison's disease, allergies, autoimmune confidence, autoimmune thyroiditis, diabetes mellitus, Crohn's cardiovascular disorders such as myocardial ischaemias; wound healing; inference, and elegans and epilepsy; and cardiang; and epilepsy; and cardiovascular disorders such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뭐
       Sequence 549
                                                                    infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1142-1144; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US005881.
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                                                                                                                                                                          380 ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY 439
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                                                                                                                                                                                                                                                                     266 LEAHDYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELLITLSQKTKSFTRVVDGA 323
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                                                                                                 EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-10-023-515-2
US-9-595-682B-26
US-09-949-016-6426
US-09-949-016-9670
US-09-595-682B-21
US-09-595-682B-26
US-09-6845-295A-2
US-09-146-661-2
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APPLICANT: Dotter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth (
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: 00/075,258
PRIOR APPLICATION NUMBER: POT-19
PRIOR APPLICATION NUMBER: POT-19
PRIOR APPLICATION NUMBER: POT-19
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 554
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Best Local :
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ORGANISM: Homo sapiens
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39.9%; Score 1230; DB 4; Length 559;
Local Similarity 46.7%; Pred. No. 4.8e-125;
hes 248; Conservative 91; Mismatches 168; Indels 2
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                                                                                                                                                                                                         VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHXAIMESGVAIIPY 265
                                                                                                                                                                                                                                                      ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
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                                                                   FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
                                                                                                          LIA----SSADVISTVVANLSACDQVDSEALVGCLRGKSKEEILAINKPFKMIPGVVDGV
                                                                                                                                                                                VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
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ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6426
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Patent No.
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APPLICANT: VENTER, J.
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TYPE: PRT
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                       EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                                                                                                                                                                                                                     FFPNEPLDILSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN 379
                                                                           LLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY
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                                                                                                                                                                                                                                                                                               VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                             RDGTTHPAMCLQDLTAVESEFL----SQFNMTFPSDSMSEDCLYLSIYTPAHSHEGSNLP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFARTGNENGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEDRVDFWTSTIP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEEQLSRKMKYWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKYWA 499
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46.7%; Pred. No. 4.8e-125;
ative 91; Mismatches 168;
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; LENGTH: 577
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9670
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOPTWARE: FABSEQ for Windows Version 4.0
SEQ ID NO 9670
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US-09-949-016-9670

; Sequence 9670, Application US/09949016

; Patent No. 6812339

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: POLYMORPHISMS, METHODS OF DETECTION AND USES THEREOF
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Best Local S
Matches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REATSYPHICLON----SEWILLDOHMLKVHYPKFGVSEDCLYLHIYAPAHADTGSKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPESWSGV
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BFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                             ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                                                                                                                     FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
                                                                                                                                                                                                                                                                                                               LEAHDYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGA
                                                                                                                                                                                                                                                                                                                                                              VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
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                                   TFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP 550
                                                                       EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEEQLSRKMMKYWA
                                                                                                                                         LLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY
                                                                                                                                                                                                                  FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT 395
                                                                                                                                                                                                                                                                                      LIA----SSADVISTVVANLSACDQVDSBALVGCLRGKSKEEILAINKPFKMIPGVVDGV
                                                                                                                                                                                                                                                                                                                                                                                                VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                     VMVWIHGGALVFGMASLYDGSMLAALENVVVVIIQYRLGVLGFFSTGDKHATGNWGYLDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.9%; Score 1230; DB 4; 46.7%; Pred. No. 5.1e-125; tive 91; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
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RESULT 5 US-09-595-682B-21

RESULT 6
US-09-264-737-2
; Sequence 2, Application US/09264737A
; Patent No. 6107549
; GENERAL INFORMATION:

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APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION UNMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
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LENGTH: 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 WCFFLILOPLIGHROWGKTGPSAEGPORNTRIGWIOGKOVTVLGSPVPVNVFLGVPFAAP
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                                                                                                                                                                    NEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTK
                                                                                                                                                                                                                                                                                                           TEEELMEVTLKMKFMALDLVGDPKENTAFLTTVIDGVLLPKAPAEILAEKKYNMLPYMVG
                                                                                                                                                                                                                                                                                                                                                                                                                           SPMAKGLFHKAIMESGVAIIPYLEAHDYEKSED--LQVVAHFCGNNASDSEALLRCLRTK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIBFFGGDPSSVTIFGESAGAISVSSLIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHML------KVHYP-KFGV
POWPAYDYKEGYLQIGATTQAAQKLKDKEVAFWT 547
                                    SIMPAYNLTEQYLOLDLNMSLGQRLKEPRVDFWT 546
                                                                                                                                                    EKYLGGTDDEVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYMYEYRYRPSFSSDMR
                                                                                                                                                                                                                                                                   VNNHECGFLLPM------KEAPEILSGSNKSLALHLIQNILHIPPOYLHLVA 392
                                                                                                                                                                                                                                                                                                                                               PSKELL--TLSQK-----TKSFTRVVDGAFFPNEFLDLLSQKAFKAIPSIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIWGFFSTGDEHSRGNWGHLDQVAALRWVQDNIANFGGDPGSVTIFGESAGGQSVSILLL
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                                                                          PKTVIGDHGDEIFSVLGAPFLK-----EGATEEEIKLSKMVMKYWANFARNGNPNGEGL
                                                                                                              PAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKYWATFARTGNPNGNDL
                                                                                                                                                                                                                                                                                                                                                                                       SPLTKNLFHRAISESGVALLSSL----FRKNTKSLAEKIAIEAGCKTTTSAVMVHCLRQK
                                                                                                                                                                                                                               INQQEFGWIIPMQMLGYPLSEGKLDQKTATELLWKS-----YPIVNVSKELTPVAT
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43.9%; Pred. No. 2.5e-116;
rative 75; Mismatches 180;
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RESULT 7

US-09-595-682B-26

Sequence 26, Application US/09595682B

Patent No. 6800483

GENERAL INFORMATION:

APPLICANT: Danks, Mary K.

APPLICANT: Potter, Philip M.

APPLICANT: Houghton, Peter J.

TITLE OF INVENTION: Compositions and TITLE OF INVENTION: Tumor Cells

FILE REFERENCE: SJ-0005
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APPLICANT: Ruff, Thomas G.

TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 566
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; ORGANISM: Rabbit
US-09-264-737-2
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Best Local Similarity
Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLWPAYNLTEQYLOLDLNMSLGQRLKEPRVDFWT 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKYLGGTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYMYEYRYRPSFSSDMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQWPAYDYKEGYLQIGATTQAAQKLKDKEVAFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKTVIGDHGDEIFSVLGAPFLK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INQQEFGWIIPMQMLGYPLSEGKLDQKTATELLWKS-----YPIVNVSKELTPVAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPLTKNIFHRAISESGVALLSSI----FRKNTKSLAEKIAIEAGCKTTTSAVMVHCIRQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPMAKGLFHKAIMESGVAIIPYLEAHDYEKSED--LQVVAHFCGNNASDSEALLRCLRTK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĠĬWĠFFSTGDEHSRĠNWGHLDOVRAĹĸWVQDNĬANFĠĠDÞGSVTĬFĠĖŚAĠGQŚVŚĪĹĹĹ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEDCLYLNIYTPADLTKRGRLPVMVWIHGGGLMVGGASTYDGLALSAHENVVVVTIQYRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLF-----LAACTAWGH--PSAP-PVVDTVKGKVLGKFVSLEGFAQPVAVFLGVPFAKP
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Pred. No. 5.1e
                                                                                                                Methods for Sensitizing
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5.1e-115;
hes 176;
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                                                                                                                      Patent No. 5817490
GENERAL INFORMATION:
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ADDRESSEE: Eastman C STREET: P.O. Box 511 CITY: Kingsport

Chemical Company

Enzymatic Process for the Manufacture Ascorbic Acid, 2-Keto-L-Gulonic Acid, 2-Keto-L-Gulonic Acid

Esters

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Kingsport

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RESULT 8
US-08-845-295A-2
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CURRENT FILLING DATE: 2000-01-16;
PRIOR APPLICATION NUMBER: 60/075,258;
PRIOR FILLING DATE: 1998-02-19;
PRIOR APPLICATION NUMBER: PCT/US99/03171;
PRIOR FILLING DATE: 1999-02-12;
NUMBER OF SEQ ID NOS: 30;
SOFTWARE: PatentIn Ver. 2.0;
SEQ ID NOS: 30;
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TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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                                                           POWPAYDYKEGYLOIGATTQAAQKLKDKEV
                                                                                                                  PKTVIGDHGDEIFSVLGAPFLK-----EGATEEEIKLSKMVMKYWANFARNGNPNGEGL
                                                                                                                                    PAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDL 512
                                                                                                                                                                                                                                                                        VNNHECGFLLPM------KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVA 392
                                                                                                                                                                                                                                                                                                       TEEBLMEVTLKMKFMALDLVGDPKENTAFLTTVIDGVLLPKAPAEILAEKKYNMLPYMVG
                                                                                       SLWPAYNLTEQYLOLDLNMSLGORLKEPRV 542
                                                                                                                                                                               EKYLGGTDDPVKKKÖLFLÖMLADLLFGVPSVNVÄRHHRDAGAPTYMYEYRYRPSFSSDMR
                                                                                                                                                                                                                                          INQQEFGWIIPMQMLGYPLSEGKLDQKTATELLWKS-----YPIVNVSKELTPVAT
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COUNTRY:

Tennessee

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APPLICATION NUMBER: US 60/017,879

PILING DATE: 17-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,295A
FILING DATE: 25-April-97
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: JOURNAL FORM:
COMPUTER READABLE FORM:
TYPE: 3.5 inch disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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nes 259; Conserv
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Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES--AGAI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SEDCLYLNIYTPADLTKRGRLPVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMTSDLFTNFTGKERLTLEF-- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD------QHMLKVHYPK 120
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NFARSGNPNGEGLPHWPFTMYDQEEGYLQIGVNTQAAKRLKGEEVAFWNDLL
                                                                          QYRPSFSSDKFTKPKTVIGDHGDEIFSVFGFPLLKGD-----APEEEVSLSKTVMKFWA
                                                                                                                RHRPQCFED--TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                                                                            TVPYIVGINKQEFGWLLPTWWGFPLSEGKLDQKTATSLLWKS-----YPIANI----PE
                                                                                                                                                                                                                                                                    AIPSIIGVNNHECGFLLP-------MKEAPEILSGSNKSLALHLIQNILHIPPQ 386
                                                                                                                                                                                                                                                                                                            CLRQKSEDELLDLTLKMKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPEEILAEKDFTFN 354
                                                                                                                                                                                                                                                                                                                                              CLRTKPSKELLTLSQKTKSFT-------RVVDGAFFPNEPLDLLSQK--AFK 339
                                                                                                                                                                                                                                                                                                                                                                                     SVSVLVLSPLAKNLFHRAISESGVALTVALVRKDMKAAAKQIAVLAGCKTTTSAVFTFVH 294
                                                                                                                                                                                                                                                                                                                                                                                                           SVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQYRLGIWGFFSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDFGSVTIFGESFTAGGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILLPLYLTSLASSATW--AGQPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVFLGVPFA 59
                                  TFARTGNPNGNDLSLWP--AYNLTEQYLQLDLWMSLGQRLKEPRVDFWTSTI 549
                                                                                                                                                      ELTPVAT--PTDKYLGGTDDPVKKKDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEF
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43.8%; Pred. No. 7.4e-110;
ative 63; Mismatches 191; Indels 79;
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RESULT 9
US-09-140-933-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enz.
TITLE OF INVENTION: ASC.
TITLE OF INVENTION: 2-K
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 584 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 27-Aug CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                    local Similarity
295
                             297
                                                                                                                                                                 179
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                                                                                                                                                                                                                                                                60 KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMTSDLFTNFTGKERLTLEF--
                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                 70 APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD-----QHMLKVHYPK 120
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                                                                                                                                                 VQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES--AGAI 236
                                                              SVSVLVLSPLAKNLFHRAISESGVALTVALVRKDMKAAAKQIAVLAGCKTTTSAVFTFVH
                                                                                                                                                                                                                               FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYED--VLVVV 178
                                                                                                                                                                                                                                                                                                                                 WILLPLVITSLASSATW--AGOPASPPVVDTAQGRVIGKYVSLEGLAFTQPVAVFLGVPFA 59
                                                                                                                                                                                                                                                                                                                                                                  WCFFLIIQPILGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTV--LGSPVPVNVFLGVPFA 69
                             CLRTKPSKELLTLSQKTKSFT-----
CLRQKSEDELLDLTLKMKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPEEILAEKDFTFN 354
                                                                                             SVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLR 296
                                                                                                                              IQYRLGIWGFFSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDPGSVTIFGESFTAGGE
                                                                                                                                                                                                    ---SEDCLYLNIYTPADLTKRGRLPVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVA 174
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O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-August-98
                                                                                                                                                                                                                                                                                                                                                                                                                 35.4%; Score 1091.5;
43.8%; Pred. No. 7.46
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                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                               -----RVVDGAFFPNEPLDLLSQK--AFK 339
                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-110;
                                                                                                                                                                                                                                                                                                                                                                                                    191; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 584;
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LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-146-661-2
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US-09-146-661-2
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 259; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189
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                                                                                                                                                                                                                                                                                                                         TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: 03-Septmeber-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzyme
TITLE OF INVENTION: Ascort
TITLE OF INVENTION: Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Kingsport
                                 70 APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD------QHMLKVHYPK 120
                                                                                                                  12 WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTV--LGSPVPVNVFLGVPFA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 NFARSGNPNGEGLPHWPFTMYDQEEGYLQIGVNTQAAKRLKGEEVAFWNDLL 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 WLLPLVLTSLASSATW--AGQPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVPLGVPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
KPPLGSIRFAPPOPAEPWSFVKNTTSYPPMCCODPVVEOMTSDLFTNFTGKERLTLEF--
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                                                                                                                                                                Conservative
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03-Septmeber-98
                                                                                                                                                                                   43.8%;
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                                                                                                                                                          ; Score 1091.5; DB 3;
; Pred. No. 7.4e-110;
63; Mismatches 191;
                                                                                                                                                                                                    DB 3;
                                                                                                                                                            Indels
                                                                                                                                                                                                Length 584;
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US-09-150-515-2
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                                                        APPLICATION NUMBER: US/09/150,515

FILING DATE: 09-SEP-1998

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECHMUNICATION INFORMATION:
TELECHONE: 423-229-6189
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          TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09150515
Patent No. 6271006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFARSGNPNGEGLPHWPFTMYDQEEGYLQIGVNTQAAKRLKGEEVAFWNDLL 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVPYIVGINKQEFGWLLPTMMGFPLSEGKLDQKTATSLLWKS-----YPIANI----PE
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Ascorbic Acid, 2-Keto-L-Gulonic Acid,
2-Keto-L-Gulonic Acid
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TYPE: Amino Acid

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                                                    SEQ ID NO 1
LENGTH: 539
TYPE: PRT
ORGANISM: Rabbit
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09264737A Patent No. 6107549
Query Match
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                                                                                                                         TITLE OF INVENTION: Engineering Plant Resistance to Pyridines TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21 (10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11

SOPTWARE: Patentin Ver. 2.0
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RESULT 13
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CILASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               CITY: Fairfax
STATE: VA
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; Sequence 28, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mu
CORRESPONDENCE ADDRESS:
ANDERSES: ADDRESS:
                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-446-100-28
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Best Local Similarity 44.9%; Pred. No. 9.5e-94;
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TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterase
COMPUTER READABLE FORM:
             STREET: 9669 A
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: br
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
                                                                                                         ADDRESSEE: Hendricks and Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVRFVFGGAFLKGDIVMFEGATEBEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTE 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKKKDLILDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHAD 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELFSVFGAPFLK-----EGASEEEIRLSKMVMKFWANFARNGNPNGKGLPHWPEYNQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKQEFGWLIPMQLMSYPLSEGQLDQKTAMSLLGSPIPLFAIAKELIPEATEKYLGGTDDT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNHECGFLLPMKEAPEILSGS--NKSLALHLIQN---ILHIPPQYLHLVANEYFHDKHSL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEELLETTLKIGNSYLWTYRETQRESTLLGTVIDGMLLLKTPEELQRERNFHTVPYMVGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAKNIFHRAISESGVALTSVLVKKGDVKPLAEQIAITA---GCKTTTSAAMVHCLRQKT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMAKGLFHKAIMESGVAIIPYLEAHDYEK---SEDLQVVAHFCGNNASDSEALLRCLRTKP 302
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                                                                                     9669 A Main Street, P.O.
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                                                                                       Box 2509
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RESULT 15
US-08-446-100-30
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Best Local Similarity 44.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
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NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: brook
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: YES
FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: huma
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HYPOTHETICAL: Y
ANTI-SENSE: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                               358
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                                                                                                                                                                                                                                                                                                                                                                                                 178 EEELLETTLKIGNSYLWTYRETQRESTLLGTVIDGMLLLKTPEELQRERNFHTVPYMVGI 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 IFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 EDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLG
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                                                                                 GYLQIGANTQAAQKLKDKEVAFWTN 436
                                                                                                                     QYLOLDLIMSLGORLKEPRVDFWTS 547
                                                                                                                                                                                                                                                                              TEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHAD 462
                                                                                                                                                               ELFSVFGAPFLK-----EGASEEEIRLSKMVMKFWANFARNGNPNGKGLPHWPEYNQKE
                                                                                                                                                                                                EVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTE 522
                                                                                                                                                                                                                                        VKKKDLILDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGD
                                                                                                                                                                                                                                                                                                                     NKQEFGWLIPMQLMSYPLSEGQLDQKTAMSLLGSPIPLFAIAKELIPEATEKYLGGTDDT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                           SKELLTLSQK------TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGV 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IWGFFSTGDEHSRGNWGHLDQVAALRWVQDNIASFGGNPGSVTIFGESAGGESVSVLVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHCLYLNIYTPADLTKKNRLPVMVWIHGGHLEVGAASTYDGLALAAHENVVVVTIQYRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLAKNLFHRAISESGVALTSVLVKKGDVKPLAEQIAITA---GCKTTTSAAMVHCLRQKT 177
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YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 942.5; DB 3;
%; Pred. No. 9.5e-94;
65; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 broomfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #1.25
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Sequence 30, Application US/08446100 Patent No. 6001625

GENERAL INFORMATION:
APPLICANT: Broomf
APPLICANT: Millar

Broomfield, Millard, Cha

Clarence

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US-08-446-100-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hendricke, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9669 A
CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                              178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 QYLQLDLNMSLGQRLKEPRVDFWTS 547
                                                                                                                                 298 VKKKOLILDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                          245 PMAKGLFHKAIMESGVAIIPYLEAHDYEK--SEDLQVVAHFCGNNASDSEALLRCLRTKP 302
                                                                                                                                                        TEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHAD 462
                                                                                                                                                                                                                                           NNHECGFLLPMKEAPEILSGS--NKSLALHLIQN---ILHIPPQYLHLVANEYFHDKHSL 402
                                                                                                                                                                                                                                                                                                                                                     SKELLTLSQK------TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGV 347
                                                                                                                                                                                                                                                                                                                                                                                              ELFSVFGAPFLK-----EGASEEEIRLSKMVMKFWANFARNGNPNGKGLPHWPEYNQKE 411
                                                                                     EVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWKYWATFARTGNFNGNDLSLWPAYNLTE 522
                                                                                                                                                                                                                      NKQBFGWLIPMQLMSYPLSEGQLDQKTAMSLLGSPIPLFAIAKELIPEATEKYLGGTDDT 297
                                                                                                                                                                                                                                                                                                           EEELLETTLKIGNSYLWTYRETORHSTLLGTVIDGMLLLKTPEELORERNFHTVPYMVGI 237
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9669 A Main Street, P.O. Box 2509
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Search completed: June 15, 2005, 09:43:54 Job time : 30 secs



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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q-/Ggn2 1/USPTO_spool/664091/runat_14062005_133640_10461/app_query.fasta_1.775
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DEPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN ITMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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DB seq length: 2000000000
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Match Length DB
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0244	C0244		78		233	
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ALIGNMENTS

Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	RESULT 1 AR438765 LOCUS DEFINITION ACCESSION VERSION
cores: ilarity: Similarity:	Unknown. Unknown. Unclassified. 1 (bases 1 to 1746) Curtis,R.A.J. and S: 53010, a human carbe Patent: US 6664091-/ Location/Q 1. 1746 /mol_type=	AR438765 Sequence 3 AR438765 AR438765.1
3.08e-252 3079.00 100.00\$ 100.00\$ 100.00\$	Unknown. Unknown. Unclassiied. Unclassiied. (bases 1 to 1746) Curtis,R.A.J. and Silos-Santiago,I. 53010, a human carboxylesterase fam Fatent: US 6664091-A 3 16-DEC-2003; Location/Qualifiers 1. 1746 /organism="unknown" /mol_type="genomic DNA"	1746 bp AR438765 Sequence 3 from patent US 6664091 AR438765 AR438765.1 GI:42663740
Length: Matches: Conservative: Mismatches: Indels: Gaps:	Unknown. Unknown. Unclassified. Unclassified. (bases I to 1746) 1 (bases I to 1746) 53010, a human carboxylesterase family member and uses thereof patent: US 6664091-A 3 16-DEC-2003; Location/Qualifiers 1. 1746 /organism="unknown" /mol_type="genomic DNA"	1746 bp DNA JS 6664091.
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                              Ly8ProSerLy8GluLeuLeuThrLeuSerGlnLy8ThrLy8SerPheThrArgValVal
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                                                                                                                            AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTT
                                                                                                                                                            CTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTG
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AUTHORS
TITLE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                           Patent: WO 0250256-A 3 27-JU
Millennium Pharmaceuticals,
Location/Qualifiers
                                                                    Curtis,R.A. and Silos-Santiago,I. 53010, a novel human carboxylesterase thereof
                                                                                                                                          AX600126 1746 bp
Sequence 3 from Patent W00250256
AX600126
AX600126.1 GI:28400192
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                           27-JUN-2002;
                                                   Inc. (US)
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B1 AlaHisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThr 3	241 LeuIleLeuSerPrometAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyVal 260	CAAGGA Prose	81 TyrArgLeuGlyIlePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTrp 2	61 SerilePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGln 1 	41 GlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAla 1	21 PheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThr 1 	01 LeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLys 1 	81 ProGlnProAlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeuCys 100	61 AsnValPheLeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsn 80	41 ThrArgLeuGlyTrpIleGlnGlyLy8GlnValThrValLeuGlySerProValProVal 60	21 LeuLeuGlyHisArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsn 40 	1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCysPhePheLeuIleLeuGlnPro 20	6 Gaps: 3-2 (1-581) x AX600126 (1-1746)	t Scores: 3.08e-252
<u>.</u>														
ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	AR438764 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	ن ب	р р	Q	Db Q7	Qγ 1	D 29	рь 1	· •	μ	H	н	ц	හි පි හි
	AR438764 2158 bp DNA linear PAT 20-FEB-2004 Sequence 1 from patent US 6664091. AR438764 AR438764.1 GI:42663739 Unknown.	581 Pro 581 		521 ThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluPro 540	501 PheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeu 520 	481 GluGlyAlaThrGluGluGluLy8LeuLeuSerArgLy8MetMetLy8TyrTrpAlaThr 500 	461 AlaAspGluValArgPheValPheGlyGlyAlaPheLeuLySGlyAspIleValMetPhe 480 	441 PREATGRIBATGRIDO SEPTEMBELINE SEPTEMBELINE SEPTEMBELS SEPTEMBE	PTOALBLEULIETNIKALBATGIYYKIBSATGABBALGGIYKIBFTOVALIYFFNELYTGLU	TCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTG		Alarrodiuileueusetuiysetasuuyssetueualaleualasuuleudileliiiiiiiiiiiiiiiiiiiiiiiiiiiiii	ATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAG	321 AspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSerGlnLysAlaPheLysAla 340 961 GATGGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCA 1020 341 IleProSerIleIleGlyValAsnAsnHisGluCysGlyPheLeuLeuProMetLysGlu 360

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GlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAla
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CE 1 (bases 1 to 2047)

1 (collins, F.S., Grouse, L.H., Derge, J.G., RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Histeh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., McZernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A., Fahey, J., Helton, E., Ketteman, M., Wadan, A. C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

ED 1247932
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Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IBBR Plate: 4 Row: e Column: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                         Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Director MGC Project.
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Homo sapiens hypothetical protein FLJ31547, mRNA (cDNA clone
MGC:97182 IMAGE:7262427), complete cds.
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                                                                                                                                                    e, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
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                                            GlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyr
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KHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVFFYEFRHRPQCFEDTKPAFV
KADHADEVERVFGGAFLKGDIVMFEGATEEKLLSRKMKXYMAIFBARTGNPNGNDLSL
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WPANNLTECYLQLLMMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLSLL
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/tissue_type="PCR rescued clones"
/clone_Tib="NIH_MGC_277"
/note="Vector: pPCR-Script Amp SK(+) with reversed insert"
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SerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThrIleProLeu
                                                      LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet
                                                                                                                                                                                  TTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAAGTTACTGAGC
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                                                                                       GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu
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                                                                         CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
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                                                                                                             GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTG
                                                                                                                                 AlaPheLeuLy8GlyAspIleValMetPheGluGlyAlaThrGluGluLysLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consorthum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: k Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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Strausberg,R.

Direct Submission

Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5174937"
/tissue_type="Brain, Lung, T
/clone_lib="NIH MGC 115"
/lab_host="DH10B"
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93.59%
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JOURNAL Pat	•			AX746724 AX746724 LOCUS DEFINITION Sec	52	1792	1732	530	Oy 510 <i>I</i>	1612	1552	1492	1432 450	1372	1312	1252	1192	Qy 350 I	30	Db 1072 <i>I</i>	
Full-length clnA sequences Patent: EP 1308459-A 249 07-MAY-2003; Helix Research Institute (JP) ; Research Association for	io,Y., Otsuka,K., Nagai,K., Irie,R., hikawa,T., Otsuka,M., Nagahari,K. and	ryota; Metazoa; Chordata; Cran llia; Butheria; Primates; Cata lia; Eurivama T Otanki T	746724.1 GI:32130991 mo sapiens (human) mo sapiens	2092 bp mRNA linear PAT 20-JUN-2003 Sequence 249 from Patent EP1308459. AX746724	TCTCTCCAGCCTTTCTTTTCTTTTGTGCTCCT 1887	CTCTTTCTTCCTTAACTTTCCTC	ACATGAGCCTTGGACAGAGACTCAAAGAACCGCGGGTGGAGTTTTGGACCAGCACCATC 1791		AsnAspleuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspleu 529									CTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC	LeuAspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsn 349	AGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	

Qy 240 rLeuileLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyVa 260	220 yGlyAspProSerSerValThrIlePheGlyGluSerAlaGlyAl 	Qy 180 nTyrArgLeuGlyIlePheGlyPheFhrThrTrpAspGlnHisAlaProGlyAsnTr 200	160 aSerIlePhe 537 CTCCATCTTT			QY 100 BLEUGInAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLy 120	Oy 84 AlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeu	Qy 64 LeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsnProGlnPro 83	Qy 44 GlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProValProValAsnValPhe 63	Qy 24 HisArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsnThrArgLeu 43	6 Gaps: 5-2 (1-581) x AX746724 (1-2092)	No.: It Sim Nocal Match	Scores:	ή σ
RESULT 9 AK090997 AK090997 AK090997 AK090997 AK090997 AK090997 ACUS DEFINITION HOMO SAPIENS CDNA FLJ33678 fis, clone BRAWH2002191, weakly similar to FAITY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (EC 3.1.2.14). VERSION AK090997.1 GI:21749268 KEYWORDS ORGANISM HOMO SAPIENS (human) ORGANISM HOMO SAPIENS (human) CRGANISM HOMO SAPIENS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	Oy 580 aPro 581 Db 1797 TCCT 1800	Qy 540 oArgValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAspMetLeuHi 560	Qy 520 uThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluPr 540 	Qy 500 rPheAlaArgThrGlyAsnDroAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLe 520	Qy 480 eGluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaTh 500	QY 460 8AlaAspGluValArgPheValPheGlyGlyAlaPheLeuLy8GlyAspIleValMetPh 480	Qy 440 uPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHi 460	Qy 420 lProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrG1 440	QY 400 sSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValVa 420	Qy 380 eLeuhisIleProProGlnTyrLeuhisLeuValAlaAsnGluTyrPheHisAspLysHi 400 	Db 1137 GGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACAT 1196	340 1077	QY 320 laspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSerGlnLyaAlaPheLyaAl 340	Qy 300 rLysProSerLysGluLeuLeuThrLeuSerGlnLysThrLysGerPheThrArgValVa 320

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TITLE
JOURNAL
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AUTHORS
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Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
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Kumagai,A., Itakura,S., Puliwara,T., Ono,T., Yamada,K., Fujii,Y.,
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Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T.,
Noguchi,S., Tich,T., Shigeta,K., Senba,T., Matsumhima-Sugano,J.,
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3 (bases 1 to 2092)

3 (bases 1 to 2092)

3 Sirect Submission

Direct Submission

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K.,
Masuho,Y., Nagai,K. and Isogai,T.
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                                           /protein_id="BAC03565.1"
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TGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQK NIBFFGGDPSSVTIFGESAGAISVSSLILSFWAKGLFHKAIMESGVAIIFYLEAHDYE KSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTILSGYKTKS FTRVVDGAFFRNEFL DLLSQKAFKAIPSIGYNGHEGGFLLPMKEAPEILSGSNKSLALHLIQNILHIFPQYL HLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQ GFEDTKPA FVKADHADBVRFVFGGAFLKGDIMFEGAFEEKLLSRKMKYWATFART GNPUNDLSLWAPAYNLTEQYILQLDLMMSLGQRLKEPRVEFWTSTIPLILSASDMLHS PLSSLTFLSLLQPFFFFCAP"

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lAlaHisPhe	GGCCATCATC	AlaIleIle	rLeuIleLeu CTTATACTG	yGlyAspPro TGGGGACCCC	pAlaPheLys GGCCTTCAAG	nTyrArgLeu GTACCGGCTA	aSerIlePhe	rGlySerLy8 AGGCTCCAAG	sPheGlyVal	sLeuGlnAsn CCTCCAGAAC	AlaSerProT	LeuGlyValP	GlyTrpIleGlnGlyLys	HisArgGlnTrpG	2 (1-581)	es: rity: ilarity:
CysGlyAsnAsr	CCTTACCTGGAGGCCCA	ProTyrLeuGlu	leLeuSerProMetAlaLys	roSerSerValThrIlePheGlyGluSe 	pAlaPheLy8AspGlnValAlaAlaLeuSerTrpValGlnLy8AsnIleGluPhePheGl 	rArgLeuGlyIlePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTr 	SerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGl 	rGlySerLysLeuProValLeuValTrpPhe 	PheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAs 	LeuGlnäsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLy 	roTrpAspAsnLeuArgGluAlaThrS CTGGGATAACTTGCGAGAAGCCACCT	alProPheAlaAlaProProLeuGlySerLeuArgPheThrAsn 	lnGlyLysGln\ aGGGCAAGCAAC	З1уҍув	x AK090997	6.16e-235 2877.00 98.40% 98.04% 93.44%
mAlaSerAspS	GCCCATGATT	AlaHisAsp?	ALYSGLYLeui AAAGGCTTA:	CIlePheGlyC	AAlaLeuSer! GCTCTGTCC!	/PhePheThr:	LeuAlaAla?	JValTrpPhel 	LeuTyrLew CTCTACCTG	LeuLeuAsp(CTCTTAGAT(ArgGluAlaTI GAGAAGCCA(ProProLeuG	######################################	ThrGlyProSeralaGluGlyProGlnArgAsnThrA GGGCCTTCTGCTGAAGGGCACAGAGGAACACCA	(1-2092)	Length: Matches: Conservat Mismatche Indels: Gaps:
erGluAla	TGATTATGAGAAGAG	γrGluLγε	GlyLeuPheHisLysAlaIleMetGluSe 	luSerAla	TrpValGln GGGTCCAG	ThrTrpAsp \CATGGGAT	TyrGluAsp ATGAGGAC	ProGlyGlyAlaPheLysThrGly CCAGGAGGTGCCTTCAAGACTGGC	ASNI LETYT ACATCTAT	SlnHisMet		yserLeuA ATCCCTGC	ouGlySerF GGGAAGCC	laGluGlyP TGAAGGGC		; vative: ches:
LeuLeuAr	TGAGGA	rGlwAs	AlaileMe GCCATCAT	erAlaGlyAlaIleSer CCGCGGGAGCCATAAGT	LysAsnIl AAGAACAT	GlnHisAl CAGCATGC	ValLeuVa GTGCTGGT	AlaPheLy GCCTTCAA	AlaProAl GCGCCTGC	LeuLysVa CTCAAGGT	erTyrProAsnLeu- CCTACCCTAATTTGT	rgPheThr GATTTACG	rovalPro	roGlnArg CACAGAGG		2092 551 2 2 7
gCysL		pLeuGlr	tGlus GGAGA	0-6	eGlur - - CGAGT	aProc	IValv 	BThre	BH18A	1Hi87	TAAGA		Valas GTGAJ	AsnTh AACAC		
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300	896	280	260 836	240 776	220	200	180	160	140 476	120	100	83 296	236	176		

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                              HC069548 1896 bp mRNA linear PRI Homo sapitens hypothetical protein FL/31547, mRNA (cDNA MCC:97193 IMAGE:7262439), complete cds.
BC069548 GI:46854430
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTGATGAAGTCCGCTTTGTGTTTCGGTGGTGCCTTCCTGAAGGGGGGACATTGTTATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHi 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhcPhcValVa 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eLeuHisIleProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACAT
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RS Strausberg, R.L., Penigold, E.A., Grouse, L.H., Derge, J.G.,
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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, A.N., Gibbs, R.A.
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Submitted (29-APR-2004) National Institutes of Health, Mammalian Submitted (29-APR-2004), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor H
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Contact: MGC help desk
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Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match: DB:	Scores: 6.35e-212 Length: 1896 2606.00 Matches: 503 milarity: 88.77% Conservative: 3 . Similarity: 88.25% Mismatches: 6 h: 84.64% Indels: 58 9 Gaps: 2
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р У	72 ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg 91
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AX714052
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX714052 1962 bp Sequence 736 from Patent EP1293569. AX714052 AX714052.1 GI:29888980

DNA

linear

PAT 15-APR-2003

REFERENCE

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1

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3GlyLeuPhe 251 1GGCTTATTC 884	82 82	aLeuSerTrp 211 CTGTCCTGG 764	ePheThrThr 191 CTTCACCACA 704	eralaLeualaalaTyr 171 CCGCCCTGGCTGCCTAT 644	lTrpPhePro 151 GTGGTTCCCA 584		LeuLeuLeuAspGln 111 CTGCTCTTAGATCAA 464	roTrpAspAsnLeuArg 91 CCTGGGATAACTTGCGA 404	1	YLY8GlnVal 51 CAAGCAAGTC 284	YLYSThrGly 31					n for	,A., Sato,H., Ishii,S., Nagai,K., Irie,R., M., Nagahari,K. and
RES AKC LOC DEI	Qy Db	QY da	Qy Db	Qy Db	ОУ	D OY	- — - Ф. 59	D &	5 p 6	- da v	Оу	da Qy	Qy Db	da Qy	Db Qy	Qy Ob	Qy Db
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AK056109 Homo sapiens cDNA FLJ3 to FATTY ACYL-COA HYDR	LeuGlnProPhePhePhePheCysAlaPro 	euSerAlaSerAspMe rgTCTGCCTCCGACAT	euGlyGlnArgLeuLy cGGACAGAGACTCAA	erLeuTrpProAlaT\ CTCTGTGGCCAGCTTA	ysmetmetlysTyrTi AGATGATGAAATACTO	euLysGlyAspIleVa	ProAlaPheValLysAlaAspHi	ryntariovallytri	JeuGlyAspValPhePi	\snGluTyrPheHisA ATGAATACTTCCATG	AlaLeuHisLeuIleG CCCTCCATCTGATAC	31yPheLeuLeuProm 	LeuSerGlnLysAlaP TGTCTCAGAAAGCAT	InflysSerPheThrA ACAAAGTCTTTCACTC	AlaLeuLeuArgCysL	LysSerGluAspLeuc aaGaGTGAGGACCTGC	LygAlaIleMetGluS AAAGCCATCATGGAGA
1962 bp mRN FLJ31547 fis, clone HYDROLASE PRECURSOR,	eCysAlaPro 581 TTGTGCTCCT 1724	IleLeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuS	SerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThr11eProLeu	LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet	ArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsnAsp	PheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeuSer	laAspHisAlaAspGlı	n ray ya ra r r vari y r rue i y r giur ne Ar ghi sar ghroù in CyshneGiuAspinr	LeuLeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHisArgAsp	AlaAsnGluTyrPheHisAspLysHisSerLeuThrGluIleArgAspSerLeuLeuAsp 	LeuAlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeuVal 	CysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSer	LeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGlu 	LYSINTLYSSerPhefinrArgValValAspGlyAlaPhePheProAsnGluProLeuasp 	GluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSerGln	GluLysSerGluAspLeuGlnvalValAlaHisPheCysGlyAsnAsnAlaSerAspSer 	HisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAspTyr
62 bp mRNA linear Pl fis, clone NTZRIZ001010, wo E PRECURSOR, MEDIUM CHAIN (SerSerLeuThrPhe	PheTrpThrSerThr TTTTGGACCAGCACC	nTyrLeuGlnLeuAsp stacctccagctggac	JThrGlyAsnProAsn NACCGGGAATCCTAAT	aThrGluGluGluLys ACGGAGGAGGAGAAG	.sAlaAspGluValArgPheValPhe	sArgeroGinCysene	uIleThralaArgTyi aTCACAGCTCGATAT	rGluIleargaspSei rgaaatccgagacag	eProProGlnTyrLe cccgccrcagtatttc	ulleLeuSerGlySe arccrcagrggcrc	xIleIleGlyValA81 CATTATCGGAGTCAA:	.aPhePheProAsnGl !TTTCTTTCCTAATGA	rLysGluLeuLeuTh CAAGGAGCTGCTGAC	1eCysGlyAsnAsnAl CTGTGGTAACAATGC	leProTyrLeuGluAl CCCTTACCTGGAGGC
PRI 30-JAN-2004 weakly similar (EC 3.1.2.14).		LeuSerLeu 571 CTCTCTCTC 1694		LeuAsnMet 531 TTGAACATG 1574	GlyAsnAsp 511 GGGAACGAC 1514		eGlyGlyAla 471	GluAspThr 451		LeuLeuAsp 411 CTTCTGGAC 1364	1HisLeuVal 391 CACCTTGTG 1304	rAsnLysSer 371 CAACAAGTCC 1244	nAsnHisGlu 351 TAACCACGAG 1184	uProLeuAsp 331 CCTCTAGAT 1124	rLeuSerGln 311 CCTCAGCCAG 1064	aSerAspSer 291 GTCAGACTCT 1004	aHisAspTyr 271 CCATGATTAT 944

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                                                                                                                                                                  Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
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Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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72 LeuGlnProPhePhePheCysAlaPro 581 Qy	52 IleLeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuSerLeu 571 Qy	υN					1421	12 AlaGlyAlaProValTyrPheTyrGluPheArgHisArgProGluCysPheGluAsgmThr 451	AlaAsnGluTyzebeHiaAspLysHisSerLeuThrGluIleArgAspSerLeuLeuAsp	CTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTG 1304	371 1244	2 LeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGlu 351 	LysThrlysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAsp 331	GluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSerGln 311	291	252 HisLyshlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAspTyr 271	232 SerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLy8GlyLeuPhe 251 x.	765 GTCCAGAAGAACATCGAGTTCTTCGGGGGGGACCCCAGCTCTGTGACCATCTTTGGCGAG 824
211 TrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGly 230	191 ThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSer 210	171 TyrgluaspValLeuValValValGlnTyrargLeuGlyTlepheGlyPhePheThr 190	151 ProGlyGlyAlaPheLysThrGlySerAlaSerTlePheAspGlySerAlaLeuAlaAla 170 	131 ASNIIeTyralaProalaHisalaAspThrGlySerLysLeuProValLeuValTrpPhe 150 	111 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130 	44	394 CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG	51 Valty 334 GTCAC	31 274	6 Gaps: 81) x AX958392 (1-1857)	Score: 2588.50 Matches: 491 Percent Similarity: 94.62% Conservative: 1 Best Local Similarity: 94.42% Mismatches: 5 Query Match: 84.07% Indels: 23	Scores:	source 1.1857 /organism="Homo sapiens" /mol_type="unassigned DNA" /Ab_Type="unassigned DNA"	Human dru Patent: W Incyte Ge	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERRICE 1		AX958392 AX958392 LOCUS AX958392 DEFINITION Sequence 20 from Patent WO0226988.	

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CQ733044 1716 bp DNA
Sequence 18978 from Patent WOO2068579.
CQ733044
CQ733044.1 GI:42314969
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                                                                                                                                                      SerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsn
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Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other transcripts.
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                                                         TrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGly
                                                                                     ProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAla
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                                                                                                                                                                                                                                           TATGAGGACGTGCTGGTTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
                                                                                                                                      TyrGluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPheFheThr
                                                                                                                                                                 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                              Canis familiaris (dog)
Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTIGCTTGGAGAIGIGTICTTTGIGGICCCTGCACTGAICACAGCTCGATAICACAGA 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-AUG-2004) Masao Miyazaki, RIKEN, Frontier System Research, Supra-Biomolecular System Research Group; Hirosawa 2-Wako-shi, Saitama 351-0198, Japan (E-mail:mmiyazaki@postman.riken.jp, Tel:81-48-467-9619,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyazaki,M., Yamashita,T., Taira,H. and Suzuki,A. cauxin family protein published Only in Database (2004) 2 (bases 1 to 1728) Miyazaki,M., Yamashita,T., Taira,H. and Suzuki,A. Direct Submission
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ProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAla 170
                                                                AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe
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SVTIFGESAGAISVSGLVLSWARSGLEHKALTWESGVALIFERBARDDERNEDLGVIAR
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WERNSSEQYLKLDLNISVGQKLKEQEVEFWSDTLPLIMSMSTAPPGPPVPLLSLSVL
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490 1452	471 AlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeu 	
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430 1272	411 AspLeuLeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHisArg	
410 1212	391 ValalaasnGluTyrPheHisAspLysHisSerLeuThrGluIleArgAspSerLeuLeu 	
390 1152	371 SerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeu	
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350 1032	331 AspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHis ::::	
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310 912	291 SerGluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSer	
290 852	271 TyrGluLysSerGluAspLeuGlnValValAlaHisPheCysGlyAsnAsnAlaSerAsp ::::: ::: ::::	
270 792	251 PheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAsp 	
250 732	231 GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLyBGlyLeu 	
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571 LeuLeuGlnProPhePhePheCysAlaPro 581
1633 CTGATAATGTCCATGTCCACAGCACCCCCTGGTCCTCCTGTCCCCTTACTCTCCCTTTCT 1692
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Search completed: June 15, 2005, 12:01:59 Job time: 7272 secs

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ALIGNMENTS

SOURCE ORGANISM REFERENCE AUTHORS REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS RESULT 1 AK077248 REFERENCE DEFINITION Pocus JOURNAL MEDLINE JOURNAL MEDLINE TITLE AUTHORS PUBMED PUBMED Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) AK077248 2687 bp mRNA linear HTC 03-APR-200 musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031415B19 product:similar to CARROXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) full (PROCAINE ESTERASE) (METHYLBUTYRASE) [Mesocricetus auratus], full Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Co Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus HTC; CAP trapper. AK077248 AK077248.1 GI:26346111 1042159 0499374 0349636 nsert sequence. musculus (house mouse) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus HTC 03-APR-2004 Murinae; Mus. Carninci, P.,

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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2687)

6 (bases 1 to 2687)
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URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
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                                                                                                                             /note="unnamed protein product; putative similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (METHYLBUTYRASE)
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/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="11 days pregnant adult"
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translation="MPLYKLLGWLNAVACGVLLLVLHVQGQDSASPIRNTHTGQVRGS"
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|mol_type="mRNA"
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           CTCTTCCATGGTGCCATCATGGAGAGTGGAGTAGCTGTGCTCCCTGATCTTATCTCCAGC
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US-10-023-515-2 (1-581) x AK077248
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                                                                                                 GlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGly 249
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LeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHis
                                                                  GGAGAGTCAGCAGGTGGCACAAGTGTGTCTTCACATGTTGTGTCCCCATGTCCCAGGGA
                                                                                                                                                                            CGTTGGGTCCAGCAAAACATTGTCCACTTTGGAGGCAACCCTGACCGAGTCACCATTTTT
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AK033563 2661 bp mRNA linear HTC 03-APR Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030624L02 product:similar to CARBOXYLESTERASE
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Haramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murate,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murate,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sagabb,Y., Tagama,A., Takahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                 Submitted (16-UIL-2001) Yoshihide Hayashizaki, The Institute c Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-Coi, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Bequencing pipeline with 384 multicapillary sequencer genome. Res. 10 (11), 1757-1771 (2000)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in R: Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
          LeuAsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrp
                                            GATCTGAAGATGAACTTGATCCTGCCTCCCATCTCTATGTCTGAGGACTGCCTGTAT
                                                               AspGlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyr 129
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Lvhykdydiavhtfelgipeakepvgelrapapeakepurggyrdgtshenwclondnlm
Gsedlkownililppiswsedclylilvprapapeakepurggyrdgtshenwclondnlm
Gsedlkownililppiswsedclylilvprapapeakepurggyrdyndheggyldyngheggyrdgtshenwynyalgyrlgylgyrgyrdgy
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Drytifgesacgtsvsshyvspmsgglfhgaimesgyavlfdlisssemvhrivan
LSGCAAVRSTLMCCLRGKNEAEMLAINKYFKIIPGVJDEELFKHPQELMASKDFHD
VPSIIGINNDEYGWILFINDPAQKIEBITRTTLPAYLKSTALKOWLFPEGGDLMEE
YMGDTEDFETLQAQFREMKGDFMFVIPALQVAHFQRSHAPVYFYEFGHRESFFKDFME
PYYKADHGDEIFUVFGYQFGNIKLPYTEEEEGLSRRWKXRANFARHGNPNSGLFYW
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/dev_stage="adult"
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IleValMetPheGluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLys
                                                 AAGGCTGACCATGGTGATGAAATTTTCCTTGTCTTTGGCTACCAGTTC-----GGTAAC
                                                                                 LYSAlaAspHisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAsp
                                                                                                                                         TyrPheTyrGluPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheVal
                                                                                                                                                                                   ATGTTCGTGATCCCTGCACTACAAGTAGCACATTTTCAACGT---TCCCCATGCTCCTGTC
                                                                                                                                                                                                          PhePheValValProAlaLeuIleThrAlaArgTyrHiaArgAspAlaGlyAlaProVal
                                                                                                                                                                                                                                                   GGGGACACTGAGGACCCCAGAGACTCTGCAAGCACAGTTCAGAGAGATGAAGGGGGACTTC 1266
                                                                                                                                                                                                                                                                                 HisAspLysHisSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspVal 416
                                                                                                                                                                                                                                                                                                                                                                                      ACCAGAAAGACCCTGCCAGCTGTTCTA-----AAAAGCACAGCCCTAAAAATG 1161
                                                                                                                                                                                                                                                                                                                                                      IleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeuValAlaAsnGluTyrPhe 396
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GATGAATATGGTTGGATCTTCCTACGATCATGGACCCAGCTCAGAAAATAGAGGAAATA 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisGluCysGlyPheLeuLeuPro-----
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This sequence was made by sequencing genomics.
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Direct Submission
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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               (1-581)
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Location/Qualifiers
                                                                                                                                                                          /gene="CES2"
/locus_tag="HCM5231"
                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                             CCTGTCCCCAGCATCATTGGTTTCAACAATGATGAGTATGGTTGGATCGTCCCCAAAAGC
                                                   AlaIleProSerIleIleGlyValAsnAsnHisGluCysGlyPheLeuLeuProMetLys 359
                                                                                                            ValAspGlyAlaPheProAsnGluProLeuAspLeuLeuSerGlnLysAlaPheLys
                                                                                                                                                   GGCAAGAGTGAAGCAGAGATTCTGGCTATTAACAAGAACTTCCAGATGATCCCTGGTGTG
                                                                                                                                                                                                         GTGGCCAAGCTCTCTGGATGTGAGGCCGTGGACTCAGAGGCCCTGGTGCGCTGTCTGAGA
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
                                                                                                                          prepare full
Genome Res.
20499374
                                                                                                                                               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                  Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Me
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AK078953
AK078953.1 GI:26347654
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1958 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male cecum cDNA, RIKEN full-length enriched
library, clone:9130231C15 product:similar to LIVER CARBOXYLESTERASE
PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus], full insert
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Rodentia;
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Sciurognathi;
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IS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shirakki, T., Sogabe, Y., Tagama, M., Tagawa, A., Takahashi, F., Takaka, Akahira, S., Takaka, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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URL:http://fantom.gsc.riken.jp/
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1958)
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[Mesocricetus auratus] (SWISSPROT|Q64419, 78.4%ID, 100%length, match=1674)"
                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; putative similar to LIVER CARBOXYLESTERASE PRECURSOR (EC
                                                                                                                                                                                  /codon_start=1
/protein_id="BAC37476.1"
/db_xref="GI:26347655"
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/clone_lib="RIKEN fu
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                        --- GACACTTCTGAGGTGGTCTACAAGACAGTAGCCAACCTATCTGGTTGTGAAGCCACA
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AspSerGluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeu
                                               TyrGluLysSerGluAspLeu---GlnValValAlaHisPheCysGlyAsnAsnAlaSer
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MGDTEDPETLQAQFREMLGDFMFVIPALQVAHFQRSQAPVYFYEFQHLSSFIKHVRPS
HVKADHGDDVAFVFGSYLWDMNLDLTEEEELLKRWWMKYWANFARNGNPNSEGLPSWP
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                                                Homo sapiens CES2 gene, genomic survey sequence. AY414459
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			RESULT 5
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PhePhe 578	PheLeuSerLeuLeuGlnProPhePhePhePhePhe	568	Ş
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JeuSerLeu 514	MetLysTyrTzpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeu	495 1524	A 4
ArgLysMet 494	GlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMet::::::::::::::::::::::::::::::::::::	475 1476	A 8
PheLeuLys 474	PheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLys catgrgaaggcagaccarggrgaargacgttgcctttgccttttggctcctatttgrggaac	455 1416	B 8
ysproAla 454 ::: ::: \GGCCATCA 1415	ProValTyrPheTyrGluPheArgHisArgProGlnCysPheGluAspThrLysProAla	435 1356	B &
AlaGlyAla 434 CCCAGGCT 1355	AspvalPhePheValValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAla	415 1299	B 8
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/alasnasn 349 TCAACACA 1091	LeuAspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsn ::: :::	330 1032	Qy Db
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GI:39770421 (human)

1680 bp VIRTUAL

DNA TRANSCRIPT,

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This sequence was made by sequencing geno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                        Science 302 (5652), 1960-1963 (2003)
                    TCCATGCTGGCTGGAGAACGTGGTGGTGGTCATCATCCAGTACCGCCTGGGTGTC
                                   SerAlaLeuAlaAlaTyrGluAspValLeuValValValValGlnTyrArgLeuGlyIle 185
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ProArgValAspPheTrpThrSerThrIlePro
                                        AACTTTGCGAGAAATGGGAAACCCCAATGGCGAGGGTCTGCCACACTGGCCGCTGTTCGAC
                                                                                               ThrPheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsn
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                        CAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGGGCCGGGCTCTGAAGGCC
                                                                                                                                  TTC-----ACTGAGGAAGAGGAGCAGCTAAGCAGGAAGATGATGAAGTACTGGGCC
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                                                                                                                                                                                                        HisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMet 479
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                                                                                                                                                                                                                                                                                                                   ValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyr 439
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory Exploration Research Group, RIKEN Genomic Sciences
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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High-efficiency full-length cDNA cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,
                                    oGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTy 171
                                                                                                                                                                                      nHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAs 131
TGGTGGTGGACTGGTTGCAGGCATGGCTTCCATGTATGATGGATCCGTGCTGGCAGCCAC
                                                                                                                      nIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhePr
                                                                                                                                                                 GAAGATAATAAAGATGATCCTGCCTCCCTTCTCTATGTCTGAGGACTGCCTGTATCTCAA
                                                                                                                                                                                                                                                                                 uAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp---Gl 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="thymus"
/clone_lib="RIKEN full-length enriched
/dev_stage="0 day neonate"
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/mol_type="mRNA"
/strain="C57BL/6J"
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db_xref="taxon:T0090"
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                   GAACCCCAACAGTGAGGATCTACCCTACTGGCCAGCGTCAAACCAAGATGATCTGTACCT
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                                                                                                         uGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGl
                                                                                                                                                                                                                   ACTCAAGTATTTCAGGCCATGGCATGTTÄÄGGCTGÄCCACGGTGÄTGÄGCTTTACCTTAT 1422
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                                                                                                                                                                                                                                                                                                       GCAGTTCAGAGAGATGATAĠĠĠĠĀĊTTCTTAATTATAATCĊĊŤĠĊĀĊŤĊCAAGTĀĠĊĀĊĠ
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sequenced by DKFZ (German Cancer Research Center, lettle-berg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp434N0935) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp434N0935 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Car
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Mammalia; E
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lammalia; Eutheria;
(bases 1 to 2888)
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DH10B; sites NotI + SalI"
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?UNLQPAVGRALKAHRLQFWKKALPQKIQELEEPEERHTEL
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|mol_type="mRNA"
|db_xref="RZPD:DKFZp434N0935"
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Qy 324 PhePheProAsnGluProLeuAspLeuLeuSerGlnLysAlaPheLysAlaIleProSer 343	Qy 304 LysGluLeuLeuThrLeuSerGlnLysThrLysSerPheThrArgValValAspGlyAla 323 ::: ::: ::::::::	Qy 284 CysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLysProSer 303	Qy 266 LeuGluAlaHisAspTyrGluLysSerGluAspLeuGlnValValAlaHisPhe 283	Qy 246 MetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyr 265 ::::::::	Qy 226 ValThrIlePheGlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerPro 245	Qy 206 ValalahlaLeuSerTrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSer 225 :::	Qy 186 PheGlyPhePheThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGln 205	Qy 166 SerAlaLeuAlaAlaTyrGluAegValLeuValValValValGlnTyrArgLeuGlyIle 185	Qy 146 ValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGly 165	Qy 126 AspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuPro 145	106 TrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLysPheGlyValSerGlu 1 	Qy 91 ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGlu 105	71 1341	Qy 51 ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla 70	31 GlyProSerAlaGluGlyProG ::: 1221 GGCCAGGACTCAGCCAGTCCCA	38.68% Indels: 3 Gaps: x HSM803013 (1-2888)	Score: 1191.00 Matches: 242 Percent Similarity: 62.15% Conservative: 88 Best Local Similarity: 45.57% Mismatches: 161
oneID=DKF equencing /.	Braunschweig/Germanny within the cDNA sequencing consortium of the German Genome Project. This clone (DKPZp686H0466) is available at the RZPD Deutsches Ressourcenzentrum fluer Genomforschung GmbH in Berlin, Germany.	Neuherberg, GERMANY Nelecular Genome Analysis, German Ca Clone from S. Wiemann, Molecular Genome Analysis, German Ca Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (Wational Research Centre for Biotechnolog	Obanger, A., Fobo,G., Han,M. and Wiemann,S. The German cDNA Consortium Direct Submitted (22-SEP-2004) MIPS. Ingolstaedter Landstr.1. D-	Bukaryota; Metazoa; Chordata; Craniata; Vertebre Mammalia; Eutheria; Primates; Catarrhini; Homini 1 (bases 1 to 3909)		HSM806270 HSM806270 HSM806270 DEFINITION HOMO Sapiens mRNA; cDNA DKFZp686H0466 (from clone DKFZp686H0466).	94 CACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCC	Db 2634 CAGGAGGACCAATACCTGCAGCTGAACGCCTGCGGGCCGGGCTCTGAAGGCC 2693	500 ThrPheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrasn	480 PheGluGlyAlaThrGluGluGluLyBLeuLeuSerArgLyBMetMetLySTyTTpAla		Qy 440 GluPheArgHi8ArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAsp 459 ::: :::	Qy 420 ValProAlaLeuIleThrAlaArgTyrHi8ArgAspAlaGlyAlaProValTyrbheTyr 439 :::		380 IleLeuHisIleProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLys	Qy 360 GluAlaProGluIleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsn 379 :::	Db 2157 ATTGTTGGTGTCAACAACAATGAATTCGGCTGGCTCATCCCCAAGGTCATGAGGATCTAT 2216

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Query
DB:
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           166 SerAlaLeuAlaAlaTyrGluAspValLeuValValValValGlnTyrArgLeuGlyIle 185
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                                                                                                                   ValLeuValTrpPheProGlyGlyAlaPheLy8ThrGlySerAlaSerIlePheAspGly 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCAGGACTCAGCCAGTCCCATCCCGACCACACACACGGGGCAGGTGCTGGGGAGTCTT 1328
                                                                                   ĠŦĠATGĠŦĠŦĠĠATCCACĠĠŦĠĠŦĠĊĠCTTGTTTTŦĠĠĊATGĠĊŦŤĊĊTTGTATĠĀŦĠĠŦ
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                                                                                                                                                                                                                                                                                                           TrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLysPheGlyValSerGlu
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DH10B; sites_SfiIA + SfiIB"
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2682 CAGGAGGAGCATACCTGCGGCTGAACCTACAGCCTGCGGTGGGCCGGGCTCTGAAGGCC
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                                      LeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu
                                                                                      AACTTTGCGAGAAATGGGAACCCCAATGGCGAGGGTCTGCCACACTGGCCGCTGTTCGAC
                                                                                                                                 ThrPheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsn
                                                                                                                                                                                                       PheGluGlyAlaThrGluGluIysLeuLeuSerArgLysMetMetLysTyrTrpAla 499
                                                                                                                                                                                                                                                                                                       HisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMet 479
                                                                                                                                                                                                                                                                                                                                                              GAGTTCCAGCÁTCAGCCCAGCTGGCTCAAGAACATCAGGCCACCGCACATGAAGGCAGÁC 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCCTGCACTCCAAGTAGCACATTTT---CAGTGTTCCCGGGCCCCTGTGTACTTCTAC 2501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyr 439
                                                                                                                                                                                                                                                                                                                                                                                                       GluPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAsp 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGATCCCCAGACCCTCCAAGCGCAGTTCCAGGAGATGATGGCGGACTCCATGTTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheVal 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluAlaProGluIleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsn 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGAGTGGCGTGGCCCTCCTGCCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, (
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs r@mail.nih.gov
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Submitted (19-DEC-2001) National Institutes of Health, Mammalian Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mus musculus, clone IMAGE:5123923,
BC019926
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/clone="IMAGE:5123923"
/tissue_type="Liver, normal. 5
/clone_Ibb="NCI_CGAP_Li9"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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High-efficiency /
Meth. Enzymol. 3(
99279253
                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus (house mouse)
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ency full-length cDNA cloning
ol. 303, 19-44 (1999)
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6 (bases 1 to 2356)
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    LeuileLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGlyProSerAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol type="mpwa"
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contribu prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, VRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                             /tissue_type="skin"
/clone_lib="RIKEN full-length enriched
/dev_stage="6 days neonate"
                                                                                                                                                                                                                                                                    /note="hypothetical Carboxylesterases type-B containing
                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="FANTOM_DB:A030007M20"
/db_xref="taxon:I0090"
/clone="A030007M20"
                                                                                                                                                                                                                                                                 (InterPro|IPR002018,
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    ATGAAGATTCAGCTAAATCAGCGTATGATGAACCAAACCAACATCAACAAAATACTCTGG
                                                                                    CCTGTGCCCTACCTCCTAGGTGTCAACAACGCAGAGTTCGAGTGGAACTTACCTTTTCTC
                                                                                                          AlaIleProSerIleIleGlyValAsnAsnHisGlu-------
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in F Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Functional annotation of a full-length
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                                                                                                                                                                                                                                          /dev____1761
/protein_id="bac37439.1"
/db_xref="GI:26347581"
/translation="MGLYPLIKLSLAACTAWGYPSSPPVNTVKGKVLGKYVNLEGFT
/bavelgvpfakpplgslrfappppapwsprvknttsyppmcsqdavggqvlselft
QPVAVELGVPFAKPPLGSLRFAPPQPAPMSFVKNTTSYPPMCSQDAVGGQVLSELFT
NRKENIPLQFSEDCLYLNIYTPADLTKNSRLFVMVWHGGGLVVGGASTYDGLALSAH
ENVVVVTIQYRLGIWGFFSTGDEHSRGNWGHLDQVAALRWVQDNIANFGGNPGSVTIF
GESAGGFSVSVLVLSPLAKNLFHRAISESGVSLTAALITTDVKPIAGLVATLSGCKTT
                                                                                                                                                                                                                                                                             /tissue_type="colon"
/clone_lib="RIKEN full-length
/dev_stage="adult"
                                                                                                                                                                                                                                     /note="unnamed
                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                              /clone="9030604P03"
                                                                                                                                                                                                                                                                                                                                                                                                                       strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                 _xref="FANTOM_DB:9030604P03"
_xref="taxon:10090"
                                                                                                                                                                                                         e="unnamed protein product; carboxylesterase 3
|MGI:2148202, GB|NM_053200, evidence: BLASTN, 99%
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Similarity:
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GlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAla
                                                                                                     PheGlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLys 248
                                                                                                                                                                CTACGCTGGGTCCAGGACAACATTGCCCAACTTTGGGGGCAACCCAGGCTCGGTGACCATC
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LAEKSPSTVPYIVGINKQEFGWIIPTLMGYPLAEKSLLOKTANSLAKSYPTLKISEN
MIPVVAEKYLGGTDDLTKKKDLFQDLMADVVPGVPSVIVSRSHRDAGASTYMYEBEYE
PSFVSAMRPKAVIGDHGDEIFSVFGSPFLKDGASEETNLSKMVMKFWANFARNGNPN
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CP111083.1 GI:33167595
EST.
Rattus norvegicus (Norway rat)
                                                                                                              CF111083 1918 bp mRNA linear EST 23-JUL
Shultzomica04334 Rat lung airway and parenchyma cDNA libraries
Rattus norvegicus cDNA clone Contig3845 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySer---AsnLysSerLeu
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Average Phred score is 20 or better. All poor quality 20) and vector/linker sequence has been removed. High quality sequence stop: 1918.

Location/Qualifiers
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1311 Haring Hall, One Shields
Tel: 530 752 0793
Fax: 530 752 4698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dept. of Molecular Biosciences, School of Veterinary Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing and microarray development Am. J. Respir. Cell Mol. Biol. 30 (3),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mashultz@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
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  TyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHis 137
                                                                                          GTTGGAGGCAGGTTCTCTCAGAGCTTTTCACCAACAGGAAAGGAAAACATTCCTTTACAG
                                                                                                                                                                                                         GAGTCTTGGAACTTTGTGAAGAATACTACCTCCTACCCACCTATGTGCTCTCAAGATGCT
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/tissue type="adult"
/dev_stage="adult"
/clone lib="Rat lung airway and parenchyma cDNA librar
/clone lib="Rat lung airway and parenchyma cDNA librar
/note="Organ: lung; Vector: pGEM-112f(-); Site_1: Eco
/note="Organ: lung; Vector: pGEM-112f(-); Site_1: Eco
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/note="organ: lung; Vect
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Rodentia;
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Matches:
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                                                                                                                                                                                            ValValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPhe 438
                                                                                                                                                                                                                                                   ACAGATGACCCTGCCGAAAGGAACGTGTTCAAGGACTTGGTTGCAGATGTGATATTT 1303
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                                     AspHisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleVal 478
                                                                             TATGAATTTGAGTATCGCCCAAGCTTTGTATCAGCCATGAGGCCCAAGACAGTGATCGGA 1423
                                                                                                                     TyrGluPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAla 458
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TACATAGTGGGCATCAACAAGCAAGAGTTTGGCTGGATCATTCCAATGCTTATGGGCTAT 1123
  GACCATGGTGAAATCTTCTCAGTATTTGGATCTCCATTTTTAAAA------
                                                                                                                                                                                                                                                                                      LysHisSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePhe 418
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

18t Strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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1 (Dases 1 to 1826)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE014YC12"
/tissue_type="placenta"
/plasmid="pCMVSPORT_6"
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1859 bp mRNA linear HTC 18-AUG-2004
Tetraodon nigroviridis full-length cDNA.
CR641368.1 GI:51137813
HTC; cDNA; full-length; Tetraodon nigroviridis.
Tetraodon nigroviridis
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Tetraodon Tetraodon Tetraodontiformes;
Acanthomorpha; Cannthopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodontidae;
                                                                                                                                                                                                                                           Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (B-mail: sequencesope.cns.fr - Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
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/db_xref="taxon:99883"
                                                                                                                                                                       tissue_type="Liver"
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1055.00
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42.94%
34.26%
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Matches:
Conservative:
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Indels:
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ProPro-----GlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHis
                                             CACGTCTCTGGT
                                                          IleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIle ::::: ::: :::
                                                                                                                                                                                                                  LeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGluCys
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                                                                                                                                                 GlyPheLeuLeuProMetLysGluAlaPro-----
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| CAACCGCTGATGTGTTCAGGATTTAGAGGTTGCAACACAAATTATTAAAGAACTTAAT
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                                                                                                                                                                                                                                                      Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads.

More information available at http://www.genoscope.cns.fr/tetraodon.
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HTC; CDNA; full-length; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Tetraodon nigroviridis full-length
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Direct Submission
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/db_xref="taxon:99883"
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Mismatches:
Indels:
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1101 CACGTCTCTGGT-----
                                                                                                                                                                                                 333 LeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGluCys 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrpValGln 213
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                                                                                                                                                                      981 TTCCTTGAGCATGAACTTCTCACTGTGCCTTTCATGACTGGAGTCAATAATAATGAAGGT 1040
                                                                                                                                                                                                                                                                                                 313 ThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeu 332
                                                                                                                                                                                                                                                                                                                                           861 ACTGCTGATTGCATCAAGAACCTGGACGTGGAAACCATTTTACCTTTAACTAAGGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 AAGCACATGCCAGGAAACATTGGTCTTCTGGATCAGGTCCAGGCTCTGAAATGGGTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                801 CAGCCAGTGTTÁCAGTTTGTCGCAAATGTATCTGGTTGTAGCACTGAAAGCACAGAAAAG 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAATTGCTGAAAGTGGCACTGCTGCAATG---CATATATTTGCTCAAGAT---GACCCC 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGAGTGTATCTCTCCTGCTGTGCTCTCACCTCTGAGGGCCTTTTCCGCCAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeuPheHisLys 253
                                                                                  GTTGGTTACTTGCTCGGTACTTTGCTCCTAAACTGGACAGAGGGGATGGACCAGGAA 1100
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                                                                                                                                                                                                                                                           GAGTTAAGGTATCCTTTAATCACCGATGGATATTTCCTCAAAAAATCAGCAGAGAAGTTG
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  -----TTCCTGTCTGTGTTCTATCCT 1133
                                                                                                                                                                                                                                                                                                                                             920
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AlaAsmGluTyrPheHisAspLysHis	GACAAATATCTCCTCTTCACCCAGACCCCCCCA 1646	GACAAATATCT	1614	D _D
384 ProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHis		CACAATATOTO	1614	3
384 ProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHis	PheTrpThrSerThrIlePro 550	ProArgValAs		ş
	CTGGGAATTGATGCAAAGGAGCAGAATGTTTATCAGGGTTTGAAAAAA 1613	ACGGAGGAGTA		Дb
	LeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu	ThrGluGlnTy		Ş
	GGGTCTCCTAATGGACAGGGTCTTGTCCACTGGCCAAAGTATGGAGAA	TTTGCTCGCAC		DЬ
	GlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeu	PheAlaArgTh		ş
	GAAGAAGAGCAGTTGACCCAAATCATGATGAGCTACTGGGGCAAC	AGTGCGTGCAC	1434	В
	GluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThr	GluGlyAlaTh	481	ş
	TTTTTCGTATTTGGGCTTTGTTTCACAGTTTCTCACATCAATCTAAGC	GGAGATGAAAT	1374	뮍
384 1134 401 1194 421 1254 441	ArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPhe	AlaAspGluVa	461	8
384 1134 401 1194 421 1254	CCCAGTTTTCTAAAGGATAAAAGATCAAGCTTTGTTAGGAGTGACCAT	TTGCAGCATTC	1314	망
384 1134 401 1194 421 1254	ProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHis	PheArgHisAr	441	Ś
384 1134 401 1194 421	GCTGCTATTGCTCACAGAGATGCAGGTGCTCCTGTGTACCTGTATGAG	CCTGCCATTAA		Ф
384 1134 401 1194	ThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGlu	ProAlaLeuIl		Ş
384 1134 401	AACAGAGACGGGTACACTGAGGTGCTTGGAGACATGATATTTGTCATT	GATCGTGTGAA	1194	Ф
384 1134	IleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValVal	SerLeuThrGl	401	Ş
384	GAGCAGCTTAGAAAACGGATTCTTAATGAATATACAGGAACTGGGGAG	GATCCCAAAGA	1134	B
	GlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHis	ProPro		ঠ

Search completed: June 15, 2005, 13:29:40 Job time: 5297 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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-Q-/cgn2_1/USPTO_spool/6664091/runat_14062005_133641_10487/app_query.fasta_1.775
-DB-Issued patents NA -QFMT=fastap_ -SUPFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -STRATE1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6664091 @CGN 1 1 69 @runat 14062005_133641 10487 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120.-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model -DEV=xlh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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US-10-023-515-3

US-10-23-515-1

US-09-949-016-3799-

US-09-949-016-555

US-09-595-682B-27

US-09-595-682B-20

US-09-264-737-3

US-09-799-451-155

US-09-949-016-2515

US-09-949-016-2516

US-09-949-016-2516
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Sequence 3, Appli
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Sequence 557, Appl
Sequence 27, Appl
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Sequence 3, Appli
Sequence 155, App
Sequence 2515, App
Sequence 2516, Ap
Sequence 2516, Ap
Sequence 5, Appli
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ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-023-515-3
US-10-023-515-2 (1-581) x US-10-023-515-3 (1-1746)
                                                                                                                                                Alignment Scores:
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                                                                                                             Score:
                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10023515
Patent No. 6664091
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CURtis, ROTY A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                          LENGTH: 1746
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                                                     Conservative: Mismatches: Indels:
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Matches:
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1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCysPhePheLeuIleLeuGlnPro

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IleProSerIleIleGlyValAsnAsnHisGluCysGlyPheLeuLeuProMetLysGlu
                                                                                                                                                                                                                                                                                                            AspG1yAlaPhePheProAsnGluProLeuAspLeuLeuSerGlnLysAlaPheLysAla 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ly8ProSerLy8GluLeuLeuThrLeuSerGlnLy8ThrLy8SerPheThrArgValVal
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                                             AlaProGluIleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsnIle 380
                                                                                                                                                                                                                                                                     GATGGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                          AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTT
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                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96).
US-10-023-515-1
                                                                                                                                                                                                                                                                                                            APPLICANT: CURTIE, ROTY A. J.

APPLICANT: Silos-Santiago, Inmaculada

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023,515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0
Alignment Scores
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US-10-023-515-1
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Patent No. 6664091
GENERAL INFORMATION:
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APPLICATION UNMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-08	1776 581 1836 1836 9-016- 9-375 No. 6	Db 1596 Triridinicia Accide Anticità Ancide Cancide Control Co	TTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCAC AlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPhe		Qy 321 AspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSerGlnLysAlaPheLysAla 340

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; ORGANISM: Human
US-09-949-016-3799
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SOFTWARE: FastSEQ for Windows Version
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SENGTH: 2117
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Sequence 555, Application US/09949016

Patent No. 6812399

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/247,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0
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948 GAGGAGATTCTTGCAATTAACAAGCCTTTCAAGATGATCCCCGGAGTGGTGGATGGGGTC 1007
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CTGCTGATGTTGCCTCCTACATTTGGTGACCTGCTGATGGGAGAGGAGTACATTGGGGACAAT 1247
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; ORGANISM: Human
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Best Local Similarity:
Query Match:
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LysGluLeuLeuThrLeuSerGlnLysThrLysSerPheThrArgValValAspGlyAla 323
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                                  CysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLysProSer
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GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Donks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT APPLICATION NUMBER: 00/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR PRILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
US-09-595-682B-20
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GENERAL INFORMATION:
                                                                        SEQ ID NO 20
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            LENGTH: 1717
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
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            LeuArgThrLysProSerLysGluLeuLeu-----ThrLeuSerGlnLys------
                                                                                                                                           ATCCTTCTATTATCCCCCCTGACCAAGAATCTCTTCCATCGAGCAATTTCCGAGAGTGGC
                                                                                                                                                            SerLeuIleLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGly
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                                             GAGAAAATTGCCATCGAAGCTGGGTGTAAAACCACCACCTCGGCTGTCATGGTTCACTGC
                                                                     GlnValValAlaHisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCys
                                                                                             GTGGCCCTCCTTTCCAGTCTC-----
                                                                                                                   ValAlaIleIleProTyrLeuGluAlaHisAspTyrGluLysSerGluAsp-----Leu
                                                                                                                                                                                             GGAGGGGACCCAGGCTCTGTGACCATCTTTGGAGAGTCAGCAGGAGGTCAAAGTGTCTCT
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CTGCGCCAGAAGACAGAAGAACTCATGGAGGTGACATTGAAAATGAAATTTATGGCT
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; TYPE: DNA; ORGANISM: Rabbit US-09-264-737-3

LENGTH:

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APPLICANT: Feng, Paul C.C.

APPLICANT: Ruff, Thomas G.

ITITLE OF INVENTION: Engineering Plant Resistance to Pyridines via TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3
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                                                                                                                                                                                                                         Sequence 3, Application US/09264737A Patent No. 6107549
                                                                                                                                                                                                           GENERAL INFORMATION:
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282 HisPhe(808 ATCGAA(302 ProSerI	264 ProTyrLeu 760 TCCAGTCTC	244 SerProl	224 SerSerValT 640 GGCTCTGTGA	204 AspGln 580 GACCAG	184 Glyile 520 GGCATC	164 AspGly	144 LeuPro 400 CTGCCG	124 SerGluAs 340 TCTGAAGA	112 HisMet	92 GluAlaTh 238 AACACCAC	72 ProLe	52 ThrVa ::::: 118 AGCTT	32 ProSe 61 CCCTC	12 TrpCysPhe 25 TGGCTCTTC	23-515-2 (1-	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity Query Match: DB:
HisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuAr 	roTyrLeuGluAlaHisAspTyrGluLysSsrGluAs 	SerProMetAlaLyBGlyLeuPheHiBLyBAlaIleMetGluSerGlyValAlaIleIl :::	erValThrilePheGlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeu 	AspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhePheGlyGlyAspPro 	YIlePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLys ::: CATCTGGGGATTCTTCAGCACAGGAGATGAGCACAGCCGAGGGAACTGGGGTCACTTG	spG1ySerAlaLeuAlaAlaTyrGluAspValLeuValValValValQlnTyrArg 	euProValleuValTrpPheProGlyGlyAlaPheLy8ThrGlySerAlaSerIlePhe ::: 	ABPCYSLeuTy \GACTGCCTTTA	BMetLeu TATGCTCTCGGAGCT	CTC	roLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg 	ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro	roSerAlaGluGlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGlnVa 	CysPhePheLeuIleLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGly	-581) x US-09-	1.34e- 1138.5 56.62% 36.98%
AlaSerAspSe	BASPTYrGluLy	/LeuPheHisL CTCTTCCATC	eGlyGluSerA GGAGAGTCAG	uSerTrpValG 3CGGTGGGTCC	eThrThrTrpA : : : CAGCACAGGAG	aAlaTyrGluA : ::: : TGCCCATGAGA	pPheProGlyG GATCCATGGAG	TLeuAsnIleT CCTGAATATTT	CTTCACCAACA	COASILEUCYSI	rgPheThrAsnI 	roValProVal ACAGCCCGTG	roGlnArgAsnTh 	leLeuGlnPro	264-737	Ü
AspSerGluAlaLeuL	TyrGluLysSerGluAspLeuGlnValValA	/SAlaIleMetG :: BAGCAATTTCCG	hrilepheglyGluserAlaGlyAlaIleserVal	lnLysAsnIleG AGGACAATATTG	spGlnHisAlaI ::: ::: ATGAGCACAGCC	spValLeuVal\ :: ::: acgrggrggrgc	lyAlaPheLys: GTGGTCTGATG	pCysLeuTyrLeuAsnIleTyralaProAlaHisAlaAspThrGlySerLys :::	Leu	TTYTPTOASDLEUCYSLEUGIDASDSETG	ProGlnProAla CACAGCCTGCA	AsnValPheLeu 3CCGTCTTCCTG	ProglnargaenthrargleuglyTrpIleglnglyL 	LeuLeuGlyHi8ArgGlnTrpGl TTGCAGCCTGCACCGCATGGGG	(1-1701)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
euArgCysLew::: TTCACTGCCTGC	LeuGlnValVal	luSerGlyVal: AGAGTGGCGTGG	erValSerSer	luPhePheGly CCAACTTTGGA	roGlyAsnTrp GAGGGAACTGG	/alvalvalgln ::: #TGACCATTCAG	ThrGlySerAla	Hi BAl AABPThi BACCTGACAAAC	TyrProLys	GluTrpLeuLeı	SerProTrpAsj GAATCATGGAG	GlyValProPh GGAGTCCCCTT	TrpIleGlnGl ::: AAAGTCCTGGG	ArgGlnTrpGl AccGCATGGGG		1701 250 75 176 176
gThrLys 3	O—₽	Alaileile 263 :::::: GCCCTCCTT 759	SerSerLeulleLeu 243 ::: TCTATCCTTCTATTA 699	GlyAspPro 223 GGGGACCCA 639	nTrpAlaPheLyв 203 Стдессте 579	TyrArgLeu 183 TACCGCCTG 519	9 E		PheGlyVal TTT			laAlaPro CCAAGCCC	ი	YLysThrGly 3		
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izhao, Ging A. i Wang, Jian-Rui Ma, Yunqing i Yamazaki, Victori i Chen, Rui-hong i Wang, Zhiwei i Wang, Dunrui		· · · · · · · · · · · · · · · · · · ·	SULT 8 -09-799-451-155 Sequence 155, Application Patent No. 6783969	16 5	15	14 4	14 4	13 4			12 3	:	1108 GAAGGCAAACTGGACCA			
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(925)
US-09-799-451-155
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APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Ac:
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 155
LENGTH: 965
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2515
LENGTH: 2802
TYPE: DNA
ORGANISM: Human
US-09-949-016-2515
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Best Local Similarity:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILLS REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-10-08
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 GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGlu-----
                                 CCGATCGGCGAGAAACGTTTCCTGCCCCCTGAACCACCCCCATCCTGGTCGGGCATCCGG
                                                                                                                           ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro
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                                                                 ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg
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388 LeuHisLeuValAlaAsnGluTyrPheHisAspLysHisSerLeuThrGluTleArgAsp 407 ::: ::: :::	355 LeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSerLeuAlaLeu 374 ::: :::::::::::::::::::::::::::::::::	316 PheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSerGln 335		240 SerLeuIleLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGly 259	200 TrpAlaPheLysAspGinvalAlaAlaLeuSerTrpValGlnLysAspIleGluPhePhe 219 :::	160 AlaSerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspYalLeuValValValVal 179 ::::::	142 Serlys	607 AACGCCACACCTTTCCCCCCAGTGTGCCCCCAGAACATCCACACAGCTGTGCCCGAAGTC 666 106TrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLysPhe 121 107
-023-515-2 (1-581) x US-09-949-016-1017 (1-4960) 41 ThrArgLeuGlyTrpIleGlnGlyLyBGlnValT	Alignment Scores: Pred. No.: 5.99e-83 Length: 960 Score: 789.50 Matches: Percent Similarity: 51.32* Conservative: 107 Best Local Similarity: 33.72* Mismatches: 210 Query Match: 25.64* Cane: 22	m Q 2	FILLE OF INVENTION: POLYMORPHIEMS IN KNOWN GENES ASSOCIATED FILE REFERENCE: CL001307 FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016 FRIOR APPLICATION NUMBER: 60/04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILLING DATE: 2000-10-20 PRIOR FILLING DATE: 2000-10-03 PRIOR FILLING DATE: 2000-10-03	09-01 08-01 08-01 08-01	Qy 531 MetSerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThrIlePro 550 2083 CCAAGGGTCCGAGATCATTACCGGGCCACTAAGGTGGCCTTTTGGAAACATCTGGTGCCC 2142 Qy 551 LeuIleLeuSerAlaSerAspMetLeuHis 560 Db 2143 CACCTATACAACCTGCATGACATGTTCCAC 2172	507 1963 514 2023	OY 468 PheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGlu 486	Db 1672 ACACTGGTGGCACTCTTCACTGACCACCAGTGGGTGGAGCCCTCAGTGGTGACAGCCGAT 1731 Qy 428 TyrHisArgAspAlaGlyAlaProValTyrPheTyrGluPheArgHisArgProGlnCys 447

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                                                                                   GlySerAsnLysSerLeuAlaLeu---HisLeuIleGlnAsnIleLeuHisIleProPro 385
                                                                                                                                                                                                                                                                                       GluProLeuAspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyVal 347
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--GlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLys 399
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT PILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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PRIOR FILING DATE: 2000-09-08
VONTERS OF SEG ID NOS: 207012
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Alignment Scores:
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                                                                      LENGTH: 2862
TYPE: DNA
ORGANISM: Human
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		Qy 199 ABnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhe 218 ::	179 ValGlnTyr	95 95	Oy 139 AspThrGlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGly 158	Db 841 GCTAAGAAACAGGGCGAGGACTTAGCGGATAATGACGGGGATGAAGATGAAGACATCCGG 900	13 78	Qy 122 GlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHis 137	QY 106TrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLysPhe 121	Qy 92 GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGlu 105 :::	Qy 72 ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg 91 :::	Qy 52 ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro 71	Qy 36 GlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGlnVal	Qy 33	QY 26 GlnTrpGlyLysThrGlyPro 32	Qy 12 TrpCysPhePheLeuIleLeuGlnProLeuLeuGlyHisArg 25)-949-016-2516 (1-2862)	Best Local Similarity: 29.66% Mismatches: 224 Query Match: 25.40% Indels: 134 DB: 4 Gaps: 20	Length:
RESULT 12	Qy 550 ProLeuIleLeuSerAlaSerAspMetLeuHis 560	Db 2140 AAACCAAGGGTCCGAGATCATTACCGGGCCACTAAGGTGGCCTTTTGGAAACATCTGGTG 2199	2080	2020	1960	1903	1843	427 1789	<u>.</u>	QY 387 TyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHisSerLeuThrGluIleArg 406	Qy 374 LeuHißLeulleGlnäsnIleLeuHißIleProPro	ь	<u>1</u> 3	QY 315 SerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSer 334	13 2	13 2	Db 1258 GGCTCTGCTCCAGCTGGGCTGTGAACTACCAACCAGTGAAGTACACCAGC 1311	Db 1198 AGCCTCCTCACGTTGTCACATCACTCAGAGGGACTTTTCCAGAGAGCCATCATCCAAAGT 1257 Qy 259 GlyValAlaileIleProTyrLeuGluAlaHisAspTyrGluLysSerGluAspLeuGln 278	QY 239 SerSerLeulleLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSer 258

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NAME/KEY: misc_feature;
; LOCATION: (4181)...(4181)
; OTHER INFORMATION: n is not determined;
; NAME/KEY: misc_feature;
; LOCATION: (4197)...(4197);
; OTHER INFORMATION: n is not determined;
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APPLICANT: Philibert, Robert A.

APPLICANT: Binns, Edward I.

APPLICANT: Delisi, Lynn

TITLE OF INVENTION: IDENTIFICATION OF POLYMOR

FILE REFERENCE: 9465.6USI1

CURRENT APPLICATION NUMBER: US/09/491,356C

CURRENT FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: PCT/US99/09365

PRIOR FILING DATE: 1999-04-29

PRIOR PILING DATE: 1999-04-29

PRIOR PILING DATE: 1999-04-29

PRIOR PILING DATE: 1998-04-39

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TYPE: DNA
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PheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHis 460
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                                                                                               ProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGlu 440
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OPERATING SYSTEM: PC-DOS/MS-CO-SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/07/732,962A FILING DATE: 19910722
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39304/JPW TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1845 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: linear
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US-07-732-962A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION OF TITLE OF INVENTION: RECOMBINANT HI NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: John P. White, Esq. STREET: 30 Rockefeller Plaza CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Fische
                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Percent Similarity:
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Query Match:
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      SerLysGluLeuLeu--
                                         CCAGGCGGCACTGGTGGGAATGACACAGAG---CTGGTAGCCTGCCTTCGGACACGACCA
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                                                                                                                                                                      AlaHisAspTyrGluLysSerGluAspLeuGlnValValAlaHisPhe-----Cys---
                                                                                                                                                                                                                  GGGGCCTGTTCCACAGGGCCGTGCTGCAGAGCGGTGCCCCCAATGGACCCTGGGCCACG
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Mismatches:
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PCT-US92-06106-1
                                                                                                              Sequence 1, Application PC/TUS9206106
GENERAL INFORMATION:
APPLICANT: Fischer, Meir
TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STREET: 30 Rocke
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                             ADDRESSEE:
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cgcaCAggggATCCCAATGAGCCCCGAGACCCCCAGAGGCCCCACAATGGCCCCCGTACACG 1605
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                                                               E: John P. White, Esq. 30 Rockefeller Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 664-0525
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
FILING DATE: 19920722
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe 150
                                                                                                                                                                                                                                                                      ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp
  ProGlyGlyAlaPheLysThrGlySerAlaSer-----IlePheAspGlySerAlaLeu 168
                                                 AACGTGTGGACACCATACCCCCGGCCTACA---TCCCCCACCCCTGTCCTCGTCTGGATC
                                                                                                                                            TTTGAGGGCACCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGACTGCCTGTACCTC
                                                                                                                                                                         GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130
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---ThrGluGluGluLy8LeuLeuSerArgLy8MetMetLy8TyrTrpAlaThrPheAla 502
                                                                                                                       TCCACGCTC----TCCTGGCCCCTGTGGATGGGGGTGCCCCACGGCTACGAGATCGAG 1449
                                                                                                                                                      GlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAlaAspGluValArg 465
                                                                                                                                                                                                                      AlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGluPheArgHisArgPro 445
                                                                                                                                                                                                                                                             AGGAGGCCTGAGCGATGTGGTGGGCGACCACAATGTCGTGTGCCCCGTGGCCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCCGAGTTCCTGGCCGGGTGCGGGTTCGGGGTTCCCCAGGTAAGTGACCTGGCAGCC
                                                                                    PheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAla-----
                                                                                                                                                                                         GCTGGGCGACTGGCTGCCCAGGGTGCCCGGGTCTACGCCTACGTCTTTGAACACCGTGCT 1395
                                                                                                                                                                                                                                                                                                ArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThr 425
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                                                 -------ATCCCCCTGGACCCCTCTCGAAAC 1485
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Percent Similarity:
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Query Match:
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PRIOR APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-949-016-1192
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH SMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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LENGTH: 2158
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                                                                                             ATTCGCCTGAAGACCCCCGGGGGCCCTGTCTCTGCTTTCCTGGGCATCCCCTTTGCGGAG
                                                                                                                                                                                                                                                                                                                                         LeuLeuGlyHisArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsn 40
CCACCCATGGGACCCCGTCGCTTTCTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTG 364
                                            ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu 90
                                                                                                                                                                                                CTGAGGGCCGGGAGGAGCTG-CTGGTGACGGTGCGTGGGGGCCGGCTGCGGGGC
                                                                                                                                                                                                                                            ThrarqLeuGlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProVal-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLysPro 302
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                                                                                                          GAGGCTGTGGTCCTGCATTACACAGACTGGCTGCATCCCGAGGACCCCG---GCACGCCTG 1369
                                                                                                                                                                                                                                                                                                                                TTTCTG---GTTTACGGGGCCCCAGGC---TTCAGCAAAGACAACGAGTCTCTCATCAGC 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGGAGACTTCCACGGCCTGCAGGTGCTGGTGGGTGTGGTGAAGGATGAGGGCTCGTAT 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSer 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGCAGGTCCTGGTGAACCACGAATGGCACGTGCTGCCTCAAGAAAGCGTCTTCCGGTTC 1078
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                                                    ArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThr 425
                                                                                                                                                                                                                     CGGGCCGAGTTCCTGGCCGGGTGCGGGTCGGGGTTCCCCCAGGTAAGTGACCTGGCAGCC 1312
                                                                                                                                                                                                                                                                       AlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeuValAla 392
                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSerLeu---- 372
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AGGGAGGCCCTGAGCGATGTGGGGCGACCACAATGTCGTGTGCCCCGTGGCCCAGCTG 1429
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                                                                                                                                                                      Leu---ThrGluGlnTyrLeuGlnLeuAspLeuAsn---MetSerLeuGlyGlnArgLeu 537
                                                                                                                                                                                                                                            ArgThrGlyAsnProAsn------GlyAsnAspLeuSerLeuTrpProAlaTyrAsn 519
                                                                                                                                                                                                                                                                                   TACACGGCAGAGGAGAAATCTTCGCCCAGCGACTGATGCGATACTGGGCCAACTTTGCC 1639
                                                                                                                                                                                                                                                                                                         ---ThrGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAla 502
                                                                                                                                                                                                                                                                                                                                                                                            PheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAla----- 483
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                                                                                                     LysGluProArgValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAsp 557
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Search completed: June 15, 2005, 13:34:22 Job time : 331 secs

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Sequence 23, Appl
Sequence 249, Appl
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-10-142-431-5	0-035-719-	40-474-5	-10-137-865-5	US-10-036-214-22	4-2	US-10-176-921-541	-10-176-918-5	-10-175-746-5	0-140-470-54	23-904-5	-10-121-049-5	-10-140-808-5	5-855-2	-10-028-072-5	0-036-041-2	036-	-09-931-836-2	956-157-4	S-10-102-806-2	09-925-298-2	-10-843-641A-2	-10-843-6	-10-843-641A-8	-10-858-271-2	873-367C-8	S-09-873-367C-82	-09-954-531-103	09-880-107-385	-10-302-172-15	-10-451-168-	-10-233-933A-	-10-233-933A-	-10-381-898	51-168-4	-10-114-270-19	US-10-094-749-736	US-10-451-168-40
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ALIGNMENTS

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APPLICANT: CUTTIS, ROTY A. J.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERJ

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023,515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

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; TYPE: DNA
; ORGANISM: Homo Bapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1838)
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Publication No. US20020182636A1
GENERAL INFORMATION:
Query Match 100.0%; Score 2158; Best Local Similarity 100.0%; Pred. No. 0; Matches 2158; Conservative 0; Mismatches
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Sequence 1, Application US/10674636

Publication No. US20040086922A1

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.

APPLICANT: Silos-Santiago, Inmaculada

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/674,636

CURRENT FILING DATE: 2003-19-39

PRIOR APPLICATION NUMBER: US/10/023,515

PRIOR APPLICATION NUMBER: 06/256,369

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOPTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2158

TYPE: DNA

ORGANISM: Homo sapiens

PEATURE:

NAME/KEY: CDS

LOCATION: (96)...(1838)
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APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: MINCLOCICAL DISORDERS USING 4390, 54181, 211, 5687, 884,
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; NUMBER OF SEQ ID NOS: 136; SOFTWARE: FastSEQ for Wind; SEQ ID NO 45; SEQ ID NO 45; LENGTH: 2158; TYPE: DM: Homo sapiens FEATURE: Homo sapiens; NAME/KEY: CDS; LOCATION: (96)...(1841) US-10-757-262-45
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APPLICANT: ANJAWALA, Madhusudan M.; YAO, Monique G.
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HEE, Ernestine A.; DING, Li
APPLICANT: HAFALIA, April J.A.; TANG, Y. Tom
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
APPLICANT: WARREN, Bridget A.; YANG, Junming
APPLICANT: WARREN, Narinder K.; NGUYEN, Danniel B.
APPLICANT: GHAWLA, Narinder K.; NGUYEN, Danniel B.
APPLICANT: GHAWLA, Narinder K.; VANG, Junming
APPLICANT: ISON, Craig H.
APPLICANT: GHAWLA, STANGAR R.; LU, Yan
APPLICANT: GHAWLA, Narinder K.; NGUYEN, Danniel B.
APPLICANT: GHAWLA, Narinder K.; LU, Yan
APPLICANT: GHAWLA, Narinder K.; LU, Yan
APPLICANT: SON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0313 USN
CURRENT PILING DATE: 2003-05-30
CURRENT FILING DATE: 2003-05-30
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PRIOR APPLICATION NUMBER: PCT/US01/47429
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR PILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR PILING DATE: 2000-12-1
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR PILING DATE: 2001-02-01
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Best Local Similarity 99.5%;
Matches 1959; Conservative
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LENGTH: 2232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 6538080CB1
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Sequence 249, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2002-03-25
PRIOR FILING DATE: 2002-03-25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 249
LENGTH: 202
TYPE: DNA
CORGANISM: Homo sapiens
US-10-104-0-47-246
                                                                                                                      US-10-104-047-249
Query Match
Best Local Similarity
Matches 1940; Conserv
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88.8%;

; Score 1917; Di ; Pred. No. 0; 0; Mismatches

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PRIOR APPLICATION NUMBER: 60/256,369 PRIOR FILING DATE: 2000-12-18	FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF FILE REFERENCE: 10448-122001 FURRENT APPLICATION NUMBER: US/10/023,515 FURBERT FILING PARTE: 2001-12-18	ENERAL INFORMATION: APPLICANT: Curtis, Rory A. J. APPLICANT: Silos-Santiago, Inmaculada TITLE OF INVENTION. 53010 A NOVET. HIMAN CAPBOXYLESTERBASE	3ULT 6 10-023-515-3 sequence 3, Application US/10023515 sublication No. US20020182636A1			GGCAACAAGATTTTCTTCAATAATTTTGGAAGAGGGCTCGGCCTATTAGTTGTCTTAATAAT			THE TREE TREE TREE TREE TREE TREE TREE T	TERCHICATION COLOR CONTROL CON	1676 GANCISANCATGASCCICGASCANGANCCGCGGGGGGGGGGGGGGGGGGGGGGGGGG	TARTOGRAPHE AND THE CONTROL OF THE C	1516 GAAGTIACIGNOCCGANGATIANI GOOGGIACCTITEGICGANCCGGANTCC 1517 1518 GAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCC 1577 1518 GAAGTTACTGAGCCGGAAGATGATGAAGAATACTGGGCTACCTTTGCTCGAACCGGGAATCC 1577		398 CTTTCGGTGGTGCTTTCTTGAAGGGGAGGACAGTGTTTGTCAAAGCCGACGACGACGAGGAGGAGGAGGA		1278 CAGTCTTCTGGACTTGGTGGACCTTGTGTCTTTTGTGGTCCCTGCACTGATCACAGCTCG 1337	1218 TITGCACCITGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA

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# PRIOR APPLICATION NUMBER: 60/279,508
# PRIOR FILING DATE: 2001-03-28
# NUMBER OF SEQ ID NOS: 6
# SOFTWARE: FASTSEQ for Windows Version 4.
# SEQ ID NO 3
# LENGTH: 1746
# TYPE: DNA
# ORGANISM: Homo sapiens
US-10-023-515-3
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80.9%; Score 1746;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1746; Conservative 0; Mismatches
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Sequence 3, Application US/10674636
Publication No. US20040086922A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
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CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
US-10-674-636-3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1746; Conservative 0; Mismatches
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RESULT 8
US-10-451-168-40
; Sequence 40, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
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APPLICANT: SMITHKLINE BEECHAM P.1.c.
APPLICANT: GLAXO GROUP LIMITED

ITILE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP50039

CURRENT APPLICATION NUMBER: US/10/451,168

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR FILING DATE: 2000-12-17

PRIOR FILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/264,922

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR APPLICATION NUMBER: 60/266,997

PRIOR APPLICATION NUMBER: 60/266,997

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/276,988

PRIOR PILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/289,622

PRIOR APPLICATION NUMBER: 60/289,622

PRIOR APPLICATION NUMBER: 60/289,622

PRIOR PILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 110

SOFTWARE: FREESEQ for Windows Version 4.0

LENGTH: 1728
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 99.9%;
Matches 1654; Conservative
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APPLICANT: SEKI, NACHIKO

APPLICANT: YOSHIKAWA, TSUTOMU

APPLICANT: OTSUKA, MOTOYUKI

APPLICANT: NAGHIKAI, KENJI

APPLICANT: NAGHIARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

TITLE OF INVENTION: NOVEER: US/10/094,749

CURRENT APPLICATION NUMBER: US/10/094,749

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/350,435

PRIOR FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: JP 2001-328381

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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OTSUKI, TETSUJI
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SATO, HIROYUKI
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NAGAI, KEIICHI
IRIB, RYOTARO
TAMECHIKA, ICHIRO
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ISONO, YUUKO
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APPLICANT: Shimkets, Richard A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Ji, Weizhen
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APPLICANT: Liete, Mario W.
APPLICANT: Liete, Mario W.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark E.
ITILE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-332C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 500/281,136
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,863
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Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
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APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Diu, Ziaohong
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Li, Li
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Shimkets, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Casman, Stacie J.
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
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PRIOR APPLICATION NUMBER: 60/281,906

PRIOR APPLICATION NUMBER: 60/282,020

PRIOR FILING DATE: 2001-04-05

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PRIOR PRIOR APPLICATION NUMBER: 60/282,930

PRIOR PRIOR PRILING DATE: 2001-04-10

PRIOR FILING DATE: 2001-04-10

PRIOR PRIOR FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/283,512

PRIOR APPLICATION NUMBER: 60/283,710

PRIOR APPLICATION NUMBER: 60/283,710

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; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
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PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 41
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
US-10-451-168-41
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
FULE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PRILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR PRILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR PRILING DATE: 2001-02-06
PRIOR PRILING DATE: 2001-02-06
PRIOR PRILING DATE: 2001-02-06
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Best Local Similarity
Matches 1494; Conserv
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                                                ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                                                         TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
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Pred. No. 0;
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Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda, BAUGHN, Mariah R.;
APPLICANT: BOROWSKY, Mark L.; DING, Li,
APPLICANT: BOROWSKY, Mark L.; DING, Li,
APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: SANJANWALA, Madhusudan M.;
APPLICANT: SANJANWALA, Madhusudan M.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: YANG, Junning; YAO, Monique; YUE, Henry
FILE OF INVENTION. DUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR PILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/250,567
PRIOR APPLICATION NUMBER: US 60/250,567
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; OTHER INFORMATION: Incyte ID No: 7473645CB1
US-10-381-898-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.2%;
Best Local Similarity 94.7%;
Matches 1473; Conservative C
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SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 1857
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
476 CCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTT
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                                                                                                                                              GATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCT
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Pred. No. 0;
0; Mismatches
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US-10-381-898-20 RESULT 12

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APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (175)..(1803)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1804)..(2145)
OTHER INFORMATION: n is a,
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Local Similarity 78.2%;
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APPLICANT: YAMASHITA, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
LENGTH: 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Felis
US-10-233-933A-1
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US-10-233-933A-1
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Best Local Similarity 80.9%;
Matches 1265; Conservative
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                                                                      GGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGGAGTTA 1562
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                                                                                                                                              GACACGAGGCCAGCTTTCGTGAAAGCCGATCACTCTGATGAAATCCGCTTCGTCTTTGGA
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 CTGAGCAGGAAGATGATGAGGTACTGGGCCAACTTTGCTCGGACCGGGGACCCTAACGGG
                     CTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
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NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASTSEQ for Windows Ve
SEQ ID NO 42
LENGTH: 1071
TYPE: DNA
ORGANISM: Homo sapiens
US-10-451-168-42
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FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR FILLING DATE: 2000-12-19
PRIOR FILLING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILLING DATE: 2001-01-09
PRIOR PILLING DATE: 2001-01-09
PRIOR PILLING DATE: 2001-01-09
PRIOR PILLING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILLING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/276,988
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PRIOR PILLING DATE: 2001-03-19
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US-10-451-168-42
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                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.3%;
Best Local Similarity 99.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SMITHKLINE BEECHAM CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
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                                                                                                                       CATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAA
                                                                                                                                            CATTICIGIGIAACAAIGCGICAGACICIGAGGCCCIGCIGAGGIGCCIGAGGACAAAA 998
                                                                                                                                                                                                       ATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCA
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GLAXO GROUP LIMITED
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Search completed: June 15, 2005, 08:31:05 Job time: 1399.55 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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ALIGNMENTS

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GI:42663739 d. colon patent US 6664091. d. colon patent US 6664091. to 2158) to 2158 di nan carboxylesterase family member and us 6664091-A 116-DEC-2003; cation/Qualifiers 2158 rganism="unknown" ol_type="genomic DNA"	241 AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTG		1 CCACGCGTCCGAAAAACAGGCCTGGAGAGCAATGTGAGTAAGCAATGTAATAAAACGA	nown. nown. lassified. lassified. (bases 1 to 2158) tis,R.A.J. and Silos-Santiage lo, a human carboxylesterase ent: US 6664091-A 1 16-DEC-20 Location/Qualifiers 1. 2158 /organism="unknown" /mol_type="genomic DNA" milarity 100.0%; Score 211 milarity 100.0%; Pred. No Conservative 0; Mismatc	AR438764 2158 bp DNA linear Sequence 1 from patent US 6664091. AR438764 AR438764.1 GI:42663739
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AX600124 Sequence 1 from Patent WO0250256. AX600124 AX600124.1 GI:28400190 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Curtis,R.A. and Silos-Santiago,I. 53010, a novel human carboxylesterase family member and uses thereof Patent: WO 0250256-A 1 27-JUN-2002; Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers e	ACAGAGATGCTGGTGCACCTGTCTACTTCTATCATGTTTTCTATCATGTTTCTATCATGTTTCTATCATGTTTCTATCATGTTTCAAAAACACAAAAAAAA	1381 ACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTG 1440

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                         TCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTC
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NEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVFFEFRHRPQCFED
TKPAFVXADHADEVRTVPFGGAFLKGDIVMFEGATEEKLLSRKMKWAATFARTGNPN
GNDLSLWPAYNLTEQYLQLDLMNSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSL
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/mol_type="unassigned DNA"
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                                                                                                                      AAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTTCG
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                                                                  TGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCA
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416 GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCCGAGTGTCAGAAGACTG 475	356 GGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCT 415 	296 CTTTGCTGCTCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTG 355	236 GGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCC 295	176 GGGAAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	Andtch 90.5%; Score 1953; DB 6; Length 2232; Local Similarity 99.5%; Pred. No. 0; Local Similarity 99.5%; Pred. No. 0; Length 2232; Local Similarity 99.5%; Pred. No. 0; Length 2232; Lengt	/morype= unassigned nnA" /db xref="laxon:9606" /noTe="Incyte ID No: 6538080CB1"	æ	Walia, N.K., Nguyen, D.B., Gandhi, A.R. and Ison, C.H. Drug metabolizing enzymes Patent: WO 0246426-A 23 13-JUN-2002; Incyte Genomics Inc. (178)		Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutheria; Primates: Catarrhini, ucminidae.	DN Sequence 23 from Patent W00246426. N AX477711 AX477711.1 GI:22216866	AXA77711	2101 TGTAACTCATATGAAATAAAATCAGAATGTAAAATAGGAAAAAAAA	2041 CAAGATTTCTTCAATAAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATAATGGTTT 2100	1981 GGAATGATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTGGAAGGCAA 2040 		1861 TTTGGTTTCCCTTCTCCTCCCATAATTTCTCCCCGCAATCATTAGCTTCTTTCT	108
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3 (bases 1 to 2092)
1 Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Frailistics. These allocation for fill insert sequencing and
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="BRAWH2002191"
/tissue type="brain"
/clone_Tib="BRAWH2"
/note="cloning vector: pw
394. .1803
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ORIGIN Query Match Best Local Similarity Matches 1940; Conser 1016 596 918 858 968 836 678 716 819 656 558 498 438 416 978 956 798 738 536 476 378 318 366 306 198 186 258 246 TGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGAC GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA TTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGC CCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCCTGCTAGGATACTGGAATATTTTGG CCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCCTGGTACCGGCTAGGAATATTTGG GGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGC GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTG CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT TGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCCTCCAAGGAGCTGCT GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA CAMAGGCTTATTCCACAMAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA TTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGC CCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTT CGAGAAGCCACCTCCTACCCTAATTTGTAAGACCAGGTGCCTCCAGAACTCAGAGTGGCT CGAGAAGCCACCTCCTACCCTAATTT--------GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT CCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTT GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTG CCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 88.8%; ilarity 99.2%; Conservative Score 1917; D Pred. No. 0; 0; Mismatches DB -GTGCCTCCAGAACTCAGAGTGGCT 9; <u>ت</u> Length 10; 1015 955 977 917 857 677 715 617 557 595 437 415 365 305 197 797 737 497 377 257 ঠ 문 ð 밁 ð 음 성 ₽ S 문 δ 문 중 음 중 문 밁 5 닭 8 밁 8 밁 8 밁 ठ 밁 S 닭 δ 밁 δ 문 ઈ 1376 1916 1758 1638 1616 1518 1218 1256 GGTTTTGTAACTCATATGAAATAAAATCAGAATGT GGCAACAAGATTTCTTCAATAAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATAAT ACTTAGGAATGATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTGGAA GAAGTTACTGAGCCGGAAGATGATGATGATACTGGGCTACCTTTGCTCGAACCGGGAATCC ATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTG CAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCG GGTTTTGTAACTCATATGAAATAAAATCAGAATGT GCTCAGCTGCTTTCTATGGGGATCCTTGCAAAACAAGCTGCTTTCGCTGATATTTTATGG TTTCCTCTCTCCCAGCCTTTCTTTTTCTTTTGTGCTCCTTGAGAAGTTATCTTTCT GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGAGTTTTGGACCAG GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTTGGACCAG GAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCC CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTTGT CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTTGT CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCCGCCTCAGTA CAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGG CAATAGCCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGG 2092

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffbrd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnetch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
AL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing (
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Submitted (29-APR-2004) National Institutes of Health, Mammalian Submitted (29-APR-2004) National Institute, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Center code: BCM-HGSC
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Homo sapiens hypothetical protein FLJ31547, mRNA (cDNA clone
MGC:97182 IMAGE:7262427), complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian Submitted (01-NOV-2002) National Confice, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLMI at: http://image.llnl.gov Series: IRAK Plate: 51 Row: k Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2298)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5174937"
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6'
                                                                   ocation/Qualifiers
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RESULT 8 AR438765 LOCUS DEFINITION ACCESSION VERYORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE SOURCE SOURCE ORGANISM	
AR438765 AR438765 Sequence 3 from patent US 6664091. AR438765 AR438765.1 GI:42663740 . Unknown. Unknown. Unclassified. 1 (bases 1 to 1746) Curtis, R.A.J. and Silos-Santiago, I. 53010, a human carboxylesterase family member and uses thereof Location/Qualifiers Location/Qualifiers 11746	1374 CCATATACACAGATTCTTCATCACTCTTATAGACTTTCCGCCACCACCGGCCTCAG 143 1423 CONTATACACAGATTCCTTCATCACTTCTATAGACTTTCCGCCCACCGCCTCAG 1482 1434 TGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGGCTTT 1542 1434 TGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGGCTTT 1542 1436 TGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGGTTT 1542 1436 TGCTTGAAGACACGACTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAAG

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                          AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTT
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/mol_type="genomic DNA"
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thereof
Patent: WO 0250256-A 3 27-JUN-2002;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                AX600126
Sequence 3 from Patent |
AX600126
AX600126.1 GI:28400192
                                    Curtis,R.A. and Silos-Santiago,I. 53010, a novel human carboxylesterase
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                 Homo sapiens
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AX714052 AX714052 AX714052 LOCUS DEFINITION Sequence 736 from Patent EP1293569. ACCESSION AX714052 VERSION AX714052 VERSION AX714052.1 GI:29888980 KEYWORDS SOURCE Homo sapiens (human) ORGANISM EDWaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 REFERENCE 1 REGGai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,	QY 1776 AGTCCTCTTTCTTCCTTAACTTTCCTCTCTCTCCAGCCTTTCTTT		1441 1596 1501	1416 1321 1476 1381	1296 1201 1356 1261	1176 1081 1236 1141	Db 901 AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTT 960 Qy 1056 GATGGTGCTTTCCTTACCTAATGAGCCTCTAGATCTATTGTCTCAAGGAAGCATTTAAAGCA 1115 Qb 961 GATGGTGCTTTCCTTTCCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCA 1020 Qy 1116 ATTCCTTCCATCATCAGGTCAATAACCACGAGTGTGGCTTCCTGCCTACGAAGGAG 1175 Db 1021 ATTCCTTCCATCAGTCAATAACCACGAGTGTGGGCTTCCTGCTGCCTATGAAGGAG 1080

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3 (bases 1 to 1962)

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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
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Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human CDNA sequencing project
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oligo capping; fis (full insert sequence)
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Mammalia; Eutheria; Primates;
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                                     Location/Qualifiers
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shi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
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Best Local Sim
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GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCCATGGCCAAAGGCTTA
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TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC
                                                                                                       ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                                                                                                                                                                                                                                                  CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
                                                                                                                                                                                                             TATGAGGACGTGCTGGTTGTGGTCCGTCCAGTACCGGCTAGGAATATTTGGTTTCCTCCACC
                                                                                                                                                                                                                                                                       CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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ilarity 92.0%;
Conservative
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//protein_id="BAB71094.1"
//protein_id="BAB71094.1"
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PNGNDLSLKWPAYNLTEQYLQLDLNMSLGQRLKEBFRVDFWTSTIPLILSASDMLHSPLS
SLTFLSLLQPFFFFCAP"
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Pred. No. 0;
0; Mismatches
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REMARK COMMENT	REFERENCE AUTHORS TITLE JOURNAL	TITLE	AULHURO	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 12 BC069548 LOCUS DEFINITION	Qy 20 Db 19	Qy 1986 Db 1872	Qy 1926 Db 1812	Db 1752
NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Email: cgapbs-r@mail.nih.gov Tissue Procurement: Baylor Human Genome Sequencing Center cDNA Library Preparation: Baylor Human Genome Sequencing Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLLL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	896) n R-200 (MGC) nter	Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Shuffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	Klausner, R.D., Collins, F.S., Grouse, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wolley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.	BC069548 BC069548.1 GI:46854430 MCC. HOmo sapiens (human) Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1896)	BC069548 1896 bp mRNA linear PRI 30-JUN-2004 Homo sapiens hypothetical protein FLJ31547, mRNA (cDNA clone MGC:97193 IMAGE:7262439), complete cds.	046 TTTCTTCAATAAATTTGGAAGAGGGCTGGCC 2076 	86 GATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTGGAAGGCAACAAGA 2045 	126 TITCTATGGGGATCCTIGCAAAACAAGCTGCTTTCGCTGATATITTATGGACTTAGGAAT 1985	52 TTTCCCTTCTCCCCATAATTTCTCCCGCAATCATTAGCTTCTTTCT

Clone distribution: MGC clone distribution information can be found

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Query Match
Best Local Sim
Matches 1704;
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Series:
                       ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
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Location/Qualifiers
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/tissue_type="PCR rescued clones"
/clone_Tib="NIH_MGC 244"
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Pred. No. 0;
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B 8	g	g &	B 8	Qy Db	B &	B &	Query M Best Lo Matches	ORIGIN	JOURNAL FEATURES	AUTHORS TITLE	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS	RESULT 13 CQ733044 LOCUS	₽ 4	8 8 8	S B &	§ B
539 GTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCT 598	CTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGT	419 CTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCT 478	359 TAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCT 418	299 TGCTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGA 358	239 CAAGCAAGTCACTGTGGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTT 298	179 AAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	Match 66.0%; Score 1425; DB 6; Length 1716; Local Similarity 99.7%; Pred. No. 0; Les 1428; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	/db/ /mc/ /dr	Patent: WO 02068579-A 18978 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers 1 1716			CQ733044 CQ733044.1 GI:42314969		842 GATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTGGAAGGCAA 189	782	TITECTICIECTICECTATATITECTECECATATECTATION CONTROL TO THE CONTROL	
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   GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA
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Patent: WO 0226988-A 20 04-APR-2002;
Incyte Genomics, Inc. (US)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA
                                         CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA
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        Miyazaki, M., Yamashita, T., cauxin family protein Published Only in Database 2 (bases 1 to 1728)
 Miyazaki,M.,
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Canis familiaris cauxin mRNA fo
excreted protein, complete cds.
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Eutheria; Carnivora; Fissipedia; Canidae;
Yamashita, T.,
                                                                              (dog)
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                                  Taira,H.
                  (2004)
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for carboxylesterase-like urinary
                                   and
and
Suzuki
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                                                            Euteleostomi;
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Best Local Similarity
Matches 1370; Conserv
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Submitted (04-AUG-2004) Masao Miyazaki, RIKEN, Frontier System
Research, Supra-Biomolecular System Research Group; Hirosawa 2-1,
Wako-shi, Saitama 351-0198, Japan
(B-mail:mmiyazaki@postman.riken.jp, Tel:81-48-467-9619,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:81-48-467-9620
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                       ACAGGGGACCAGCACGCTCCGGGGAACTGGGCCTTCCTGGACCAGTTGGCCTTAACCC
                                                                                                  TATGAGGATGTGCTGATTGTGACAACCCCAGTACCGGCTAGGAATATTTGGTTTCTTCAAG
                                                                                                                         TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGGTTTCTTCACC
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LPFLFSSAP"
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/mol_type="mRNA"
/db_xref="taxon:9615"
/chromosome="2"
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  CTCCTCCAGCCTTTCTTTTTCTTTTGTGCTCCTTGA 1841
                                                                     ATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTTGGACCAGCACCATCCCC
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Db 1693 GTGCTCCTGCCTTCTTATTCTCCTCTGCTCCTTGA 1728

Search completed: June 14, 2005, 22:52:42 Job time: 9387.39 secs

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ADQ89093
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Adr19681 Human dru
Adc55523 Human car
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Adf59144 Cat cauxi
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Aaf55258 Nucleotid
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Adq89093 Human uro
Aad40574 Human dia
Acn42766 Human dia
Adb62095 Human cDN
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Ada53168 Human cod
Abx72267 Human NOV
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53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as
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P-PSDB; ABB79537.
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28-MAR-2001; 2001US-0279508P.
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174. .1838
/*tag= c
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/product= "53010"
/note= "the CDS is also claimed in Claim 1"
96. .173
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CC antibodies and methods for detecting the presence of 53010 potesins, fusion protesins, antigenic peptides, anti-53010 CC antibodies and methods for detecting the presence of 53010 polypeptides or nucleic acids, of identifying a compound that binds to the 53010 CC polypeptide, and of modulating the activity of the polypeptide. The 53010 CC nucleic acids and polypeptides can act as novel diagnostic and CC cherapeutic agents for controlling disorders involving aberrant or CC deficient hydrolysis of carboxylic esters. As 53010 mRNA is highly CC expressed in the central and peripheral nervous system, and its CC expression is regulated in some rodent pain models, 53010 molecules can CC also act as novel diagnostic targets and therapeutic agents for CC controlling neurological disorders, such as pain-related disorders. A CC claimed method of treating or preventing a disorder (especially a pain-CC expressing cell involves administering a compound that modulates 53010 CC activity or expression. 53010 nucleic acids are also useful in chromosome CC mapping, tissue typing, in forensic biology, prognostic assays, in and in pharmaconnemics.
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Best Local Similarity
Matches 2158; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2158 BP; 515 A; 559 C; 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surrogate markers, in tissue typing and chromosome mapping
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tive 0; Mismatches
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Use of polypeptides related to urological disorders, e.g. 44390, 5211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
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P-PSDB; ADQ89094.
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Claim 1; SEQ ID NO 45; 542pp; English

The present invention describes the use of polypeptides related to curological disorders for identifying a subject having a urological disorder. Curological disorder, identifying a subject having a urological disorder. (1) a method for identifying a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder; The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present ng a 23

Sequence 2158 BP; 515 A; 559 C; 509 ູດ 575 T; 0 U; 0 Other;

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Length

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S 밁 밁 δ 밁 문 ঠ ð á S 밁 δ 5 멍 밁 밁 밁 ঠ 밁 δ Query Match Best Local Similarity Matches 2158; Conserv 601 541 541 481 481 421 421 361 361 301 301 241 241 181 181 121 121 61 61 CCACGCGTCCGAAAAACAGGCCTGGAGAGCAATGTGGGAGTAAGCAATGTAATAAAAACGA GGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGG TAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCT TAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCT ACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCT CTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCCGCAGCCTGCATCGCCCTGGGATA CTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATA AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTG CCACGCGTCCGAAAAACAGGCCTGGAGAGCAATGTGGAGTAAGCAATGTAATAAAAACGA CTGCCTATGAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAATATTTGGTTTCT GGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGG ACCTGAACATCTATGCGCCTGCCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGT ACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGT ACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCT AAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATTGGATTCAGGGCA AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTG Conservative ; Score 2158; Pred. No. 0; 0; Mismatches 0; Indels 0, Gaps 660 360 600 360 240 180 600 540 540 480 480 420 420 300 240 300 120 120 60 60

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AAD40574 standard; CDNA; 2232 ₽P

AAD40574;

30-OCT-2002 (first entry)

Human drug metabolising enzyme (DME-10) cDNA.

Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis; proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; hanemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer; anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DMS-10; gene; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC are selected from autoimmuncy inflammatory disorder such as acquired communodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis, cc uveitis; a dell proliferative disorder such as arteriosclerosis, cc cirrhosis, hepatitis, and cancer; a neurological disorder such as control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and control and co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative neurological, developmental, endocrine, metabolic and gastrointestinal
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   GGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGC
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
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                     WPI; 2004-329368/30.
P-PSDB; ABM84114.
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New diagnostic and therapeutic polynuclectides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 1; Page; 190pp; English

The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be CC used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, or disorder, endocrine CC disorder, neurological disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 2229 BP; 503 A; 585 C; 547 G; 594 T; 0 U; 0 Other;

Matches 1955; Query Match Best Local

Similarity

89.8%;

Score 1937.4; Pred. No. 0; 0; Mismatches

DB 13; Length

Conservative

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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

Claim 1;

Page; 222pp; English.

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25-JAN-2002; 2002US-00350978.
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Otsuka M, Nagahari K, Masuho Y;
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Query Match Best Local Similarity Matches 1940; Conserv is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, ranscription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a CDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. Sequence 2092 BP; 464 A; 552 C; 497 G; 579 T; 0 U; 0 Other; 968 678 798 836 738 776 716 618 656 558 596 498 536 438 476 378 416 318 366 258 198 GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA 895 CATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGC TGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGAC TGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGAC TTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGC TTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGC CCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGG CCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCCTGGTACCGGCTAGGAATATTTTGG GGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGC GGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGC CCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTT GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGGAGTGTCAGAAGACTG GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA CATCTTT CCTCTACCTGAACATCTATGCGCCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTT CGAGAAGCCACCTCCTACCCTAATTTGTAAGACCAGGTGCCTCCAGAACTCAGAGTGGCT CGAGAAGCCACCTCCTACCCTAATTT-------GTGCCTCCAGAACTCAGAGTGGCT GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTG CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG GTCACTGTGCTGGGAAGCCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT Conservative 88.8%; Score 1917; DI Pred. No. 0; 0; Mismatches <u>,</u> DB 10; ت. '-Indels Length 2092; 10; 917 955 857 797 835 617 655 737 557 595 497 535 437 475 197 377 415 317 365 245 257 밁 Ş 문 8 밁 δ 밁 S S 뭐 밁 ð 멍 Ş 밁 Ś В S S 밁 밁 δ 밁 S S 맑 8 Ś 뫄 Ş 밁 S 밁 δ 밁 Ş 1878 1916 1818 1856 1698 1676 1578 1616 1518 1398 1338 1278 1158 1218 1256 1098 1076 978 918 956 GGCAACAAGATTTCTTCAATAAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATAAT ACTTAGGAATGATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTTGGAA GCTCAGCTGCTTTCTATGGGGATCCTTGCAAAACAAGCTGCTTTCGCTGATATTTTATGG TTTCCTCTCTCCTCCAGCCTTTCTTTTTTCTTTTTGTGCTCCTTGAGAAGTTATCTTTCT CACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCCTTCAC GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTTGGACCAG TAATGGGAACGACCTGTCT GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGAGTTTTTGGACCAG GAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCC GTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGA GAAGTTACTGAGCCGGAAGATGAAGATACTGGGCTACCTTTGCTCGAACCGGGAATCC GTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGA CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTTGT ATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTG ATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTG CAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCG TGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACCAAAACCCCTCCAAGGAGCTGCT CAGTCTTCTGGACTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCG CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTA CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTA CAATAGCCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGG TGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAAACCCCTCCAAGGAGCTGCT CAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGG 1195 2095 1997 1915 1855 2035 1937 1817 1757 1975 1877 1795 1697 1735 1637 1675 1615 1555 1457 1495 1435 1337 1375 1277 1315 1255 1577 1397 1217 1135 1517 1097 1037 977 1015

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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
            The invention relates to an isolated polypeptide with signal so which allow it to be secreted extracellularly or membrane associativity of polypeptides of the invention may be described as, cytostatic, vulnerary, antianteriosclerotic, antiparkingonian,
                                                                                                                               Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
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Best Local Similarity
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Claim 1; SEQ ID NO 736; 205pp; English.
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24-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002EP-00006586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2003
                                        polynucleotides encoding full-length polypeptides, e.g. secretory
/or membrane proteins, useful for developing medicines for diseases
ch the gene is involved, or as target molecules for gene therapy.
                                                                                                                                        2003-395539/38.
DB; ADA54807.
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Otsuka M,
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease. Sequence 1962 BP; 428 A; 541 C; 473 G; 520 T; 0 U; 0 Other, Similarity Conservative 73.2%; 0; Mismatches Score 1579.4; Pred. No. 0; DB 1; Indels 150; 10; Length Gaps

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TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
                                                                 CCAGGAGGTGCCTTCAAGACTGGCTGAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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ABX72267; ABX72267 standard; CDNA; 1746 ВP

03-JUN-2003 (first entry)

Human NOVX polynucleotide #98

Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; actric stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductue arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberous sclerosis; scleroderma, atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoletic disorder; haemophilia, hypercoagulation; Crohn's disease; cancer.

Homo sapiens.

WO200281498-A2

17-OCT-2002

03-APR-2002;

2002WO-US010780

03-APR-2001 03-APR-2001 05-APR-2001 06-APR-2001 10-APR-2001 110-APR-2001 110-APR-2001 111-APR-2001
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gorman L, Shence Padigaru M, Shi Anderson DW, Le Macdougall JR, Ellerman K;
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30-MAY-2001;
18-JUN-2001;
19-JUN-2001;
19-JUN-2001;
25-SEP-2001;
25-SEP-2001;
25-SEP-2001;
14-NOV-2001;
14-NOV-2001;
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                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerla Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ; Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
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20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0266492P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0289522P.
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Sequence 1746 BP; 401 A; 464 C; 459 G; 422 T; 0 U; 0 Other;

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cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nostropic, conductive, immunosuppressive, haemostatic, antiinflammatory, conductive, antivider, virucide, antithyroid, cerebroprotective, anorectic, conductatic, antivider, virucide, antithyroid, cerebroprotective, anorectic, conductation, replaced and polynucleotides of the invention are conducted in the treatment, or as a vaccine in the prevention of, cancer, conduction, and line disorders, infection, atherosclerosis, Parkinson's disease cound healing disorders, infection, atherosclerosis, Parkinson's disease conduction, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, configuration, systemic autoimmune disease, hyper-immunity, configuration, systemic autoimmune disease, hyper-immunity, configuration, thyroid disorders e.g. hypothyroidism, brain damages, collitis, cone phototranduction deficiency, neurological diseases, sperm dysfunction, thyroid covulation disorders, diseases in the spinal cord, thyroid gland, heart, corraches, thymus, lymph node and muscular system, obesity, anorexia, corrected sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's of the invention
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootrop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorde
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Azimzai Y, Baughin MR, Bo
Elliott VS, Gandhi AR, Gu
Lal P, Lee EA, Lu DAM, N
Ring HZ, Sanjanwala MS, J
Walsh RT, Warren BA, Xu )
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06-OCT-2000;
20-OCT-2000;
09-NOV-2000;
16-NOV-2000;
22-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; endocrine disorder; eye disorder; gastrointestinal disorder; liver disorder; metabolic disorder; gene; ds;
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S 음 성 밁 δ 뭐 ð

P-PSDB; 2002-362498/39. Borowsky ML, Ding L, Duggan BM; Griffin JA, Hafalla AJA, Ison CH, Nguyen DB, Arvizu C, Policky JL, Tang YT, Tribouley CM, Narinder W U Y, Yang J, Yao MG, Yue H; <u>.</u>

Human drug metabolizing enzymes, useful in the diagnosis and treatment disorders associated with aberrant (DME) activity, e.g., cancer and autoimmune disorders. of.

Claim 12; SEQ ID NO 20; 142pp; English.

This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a gene which encodes a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.

Sequence BP; 428 A; 487 C; 496 <u>ن</u> 446 T; Ģ 0 Other;

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P-PSDB; ADC55524.
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Polypeptide-human carboxylatase-24.64 and polynucleotide for coding
                                                                                                                                                           26-APR-2001; 2001CN-00112736.
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99.6%;
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Pred. No. 1.2e-300;
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RESULT 12
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XX JP2003250575-A. Cat cauxin encoding ADF50146 12-FEB-2004 cauxin; standard; cDNA; cat kidney disease marker; (first CDNA SEQ entry) 2145 Ħ ₽₽ NO:3. kidney disease; gene;

04-MAR-2002; 2002JP-00057908 (TOHO-) TOHOKU TECHNOARCH 04-MAR-2002; 2002JP-00057908 09-SEP-2003.

Novel ca cauxin protein or its salt, useful as or diagnosing cat kidney disease. D cat kidney disease marker,

6; SEQ ID NO 3; 33pp; Japanese.

The present sequence encodes a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosing cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin and (9) a cauxin the biological activity of urinary (I) or (VI); and (9) a cauxin cat kidney disease marker and (VI); is useful as a datection kit which measures cauxin in a test sample. (I) is useful as a disease. (I) enables detection of cat kidney disease simply and correctly. (I) provides an early marker for the disease, and replaces

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Query Match
Best Local Similarity
Matches 1466; Conserv
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                                                                              CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGGTGTCAGAAGACTGCCTCTACCTG
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         GTAGCCCTATTGACTCAAAAAGCATTTAATTCAGTTCCTTCTATCATCGGAGTCAATAAC
                  GATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCA
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                                                                                                                   GGTGATGAGAGGAAGAAGGATTTGCAGGTGCTTGCGCGTATCTGTGGTTGCCATGCGTCT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1629 BP;
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   CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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                                                    AACATCTATGCGCCAGCCCATGCGGACAATGGCTCCAACCTCCCTGTCATGGTGTGGTTC
                                                                                                                 ĊAACACGTTCTCAAAGTGCGTTACCCCAAATTGGAAGCGTCCGAAGACTGCCTGTACCTT
                                                                                                                                    CAACACATGCTCAAGGTGCATTACCCGAAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
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80.9%;
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AACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTG
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                                                                                    CTGAGCCGGAAGATGAAGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
                                                                                                                                              GGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGGAGTTA 1562
                                                                                                                                                                                                            GACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTTCGGT 1502
                                                                                                                             GGTGCCTTCCTGAAAGGCGACATTGTCATGTTCGAAGGAGCCACCGAGGAGGAGAAATTG
                                                                                                                                                                                          GACACGAGGCCAGCTTTCGTGAAAGCCCGATCACTCTGATGAAATCCGCCTTCGTCTTTGGA
                                                                                                                                                                                                                                                                                AGAGATGCTGGTGCACCTGTCTACTATGAGTTTTCGGCACCGGCCTCAGTGCTTTGAA 1442
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                                                                                                                                                                                                                                                                                                                                                                     06-FEB-2001;
19-MAR-2001;
04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
                                                                                                      Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. 'activity of polypeptides of the invention may be described as,
                                                                                                                                                                                                                                                                               (SMIK )
(GLAX )
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                                                                     2(a); Page 252;
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SMITHKLINE BEECHAM
GLAXO GROUP LTD.
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; 2001US-0260482P.
; 2001US-0264922P.
; 2001US-0266797P.
; 2001US-0276988P.
; 2001US-0281535P.
; 2001US-0289622P.
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N, Rizvi SK,
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Smith RF, Strum JC, Xie Q;
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                                                                     English.
                                                                                                         disorder.
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CC cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, CC and metabolic. Polypeptides and polynuclectides of the invention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease and polynuclectides of the invention are CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, CC inflammation, neoplastic diseases, rervous system related disorders and CC cardiovascular disorders, pancreatitis, respiratory disorder, CC hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, CC disorders e.g. hypothyroidism, brain damages, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photoctransculation desiciency, neurological diseases, stroke, angiogenesis, CC ovulation  ne
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Sequence 1071 BP; 242 A; 286 C; 254 G; 289 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 1022; Conserv

Conservative

47.3%;

Score 1021.4; DB 6; Pred. No. 4.8e-251;

Mismatches

Indels Length 1071;

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Gaps

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The invention relates to a purified human carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme and its DNA are useful for screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme
                                                                                                                                               Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication,
                                                                                                  Claim 1;
                                                                                                                                                                                                                                  WPI; 2002-195808/25
                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                              17-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; carboxylesterase-like enzyme; organophosphorus intoxication; gen osteopathic; gene therapy; osteoporosis; antisense therapy; cytostatic; detoxifying agent; Paget's disease; bone implant degradation; cancer; dental implant; enzyme; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200206454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human carboxylesterase-like enzyme cDNA.
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CC useful for treating a carboxylesterase-like enzyme dysfunction related CC disease, such as organophosphorus intoxication, cancer and osteoporosis. CC Compounds that increase the ability of human carboxylesterase-like enzyme CC to bind to organophosphorus compounds are useful as detoxifying agents. CC treating osteoporosis, Paget's disease and degradation of bone implants. CC particularly dental implants. Carboxylesterase-like enzyme is useful in CC diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of cutations in the nucleic acid sequences which encode the enzyme. The CC in gene therapy and for generating antisense oligonucleotide is useful CC in gene therapy and for generating antisense oligonucleotides or cribozymes which specifically bind to mRNA transcribed from CC useful for modulating carboxylesterase-like enzyme gene expression. The CC useful for modulating carboxylesterase-like enzyme gene expression. The CC useful for modulating carboxylesterase-like enzyme cDNA
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Best Local Similarity
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Search Job ti	В	Q	Дb	ð	рb
Search completed: June 14, 2005, 18:10:04 Job time : 1175.6 secs	827 CAGCTCAGTATCATAGAGGTG 847	1369 CAGCTCGATATCACAGAGATG 1389	767 TCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGATCCCTAAGCTGATCA 826	1309 TCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCA 1368	707 CCAATTATTTGCACCTTGTGGCTGGTGAATACTTCCATGACAAGCACTCCCTGACTGA

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ALIGNMENTS

B1922069 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181056 5', mRNA sequence. MRNA sequence. B1822069 1 GI:15933619 EST. Homo sapiens (human) EMARYOGA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo. RENCE 1 (bases 1 to 742) INH-MGC http://mgc.nci.nih.gov/. MARMALIa; Butharia; Primates; Catarrhini; Hominidae; Homo. RENAL Unpublished (1999) EMT Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov/. Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Freparation: Life Technologies, Inc. CDNA Library Inc. Prister Freparation: Life Technologies, Inc. CDNA Library Inc. Prister Freparation: Life Technologies, Inc. CDNA Library Inc. Prister Freparation: Life Technologies, Inc. CDNA Library Inc. Prister Freparation: Life Technologies, Inc. CDNA Library Inc. Prister Freparation: Life Technologies, Inc. CDNA Library Inc. Prister Freparation: Lif

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                       Submitted (16-NOV-2003) Celera Genomi
Rockville, MD 20850, USA
This sequence was made by sequencing
them based on alignment
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1680)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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 /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLNN11435 row: 1 column: 10
                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 576)
NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  quality sequence start: 6 quality sequence stop: 565 Location/Qualifiers
 /organism="Homo sapiens"
/mol_type="mRNA"
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                                                      REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
Liang, G., Miao, S.Y., Zhang, X.D., Wang, L.J. and Wang, L.F.
The differentially expressed gene in spermatogenensis
Unpublished (2002)
Contact: Lin-Fang Wang
National Laboratory of Medical Molecular Biology
Institute of Basic Medical Sciences; Chinese Academy of Medical
Sciences & Peking Union Medical College; Chinese National Human
                                                                                                                                                                                                                                                                                 BM422399 435 bp mRNA linear E4 HAS05_70 Human testis cDNA library Homo sapiens cDNA,
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                              BM422399.1
                                                                                                                                                                                            sapiens (human)
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GI:28191734

EST 01-FEB-2003 mRNA

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGT
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                                                                                                                                                                                                                                                                                                                 TCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAACACATGCTCAAGGTGCATTACCCGAAATTCGG-AGTGTCAGAAGACTGCCTCTACC
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nilarity 96.4%;
Conservative
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//lab host="DH10B"
//lab host="DH10B"
//clome_lib="NIH_MGC_115"
//clome_lib="NIH_MGC_115"
//note="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; RNA
//note="Organ: pooled brain, lung, age 23-27; 1
//note="Organ: pooled brain, lung, age 23-27; 1
//note="Organ: pooled brain, lung, age 23-27; 1
//note="Organ: pooled brain, lung, lung, age 23-27; 1
//note="Organ: pooled brain, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lung, lu
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Pred. No. 3e-101;
0; Mismatches 14;
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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            Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1680)

Clark, A. G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                         Homo sapiens (human)
Homo sapiens
                                                                                                                                                                          AY414459.1
GSS.
                                                                                                                                                                                                       AY414459
Homo sapiens CES2 gene,
genomic survey sequence.
AY414459
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#5, Dong Dan 3 Tiao, Beijing 100005, p
YongChang Road BDA, Beijing 100176, p.7
Tel: 8610-65296418
Fax: 8610-65240529
Email: wanglf@cdm.imicams.ac.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                             TGTCTTGGAAGGCAACAAGATTTCTTCAATAAATTTGGAAGAGGGCTGAC
                                                                                                                                                                                                                                                                                                                                                  TGTCTTGGAAGGCAACAAGATTTCTTCAATAAATTTGGAAGAGGGCTGGC 2075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
/tissue_type="testis"
/dev_stage="adult"
/dev_stage="adult"
/clone_lib="Human testis cDNA library"
/note="The cells of Primary Spermatocyte and Round
Spermatid were isolated from Human testis. Total RNA wa
extracted by TRIzol. Using PCR-Select cDNA Subtraction
Kit, the library was constructed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
|db_xref="taxon:9606"
                                                                                                                                                                                         GI:39770421
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99.5%;
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Pred. No. 3.7e-99;
0; Mismatches 2;
                                                                                                                                                                                                                                   1680 bp
VIRTUAL
                                                                                                                                                                                                                              DNA linear GSS 17-DE TRANSCRIPT, partial sequence,
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P.R.China
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      761
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GTGGCGTGGCCTCCTGCCCGGCCTCATTGCCAGCTCAGCTGA----
                      GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was made by sequencing them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                           ACTTTGGAGGCAACCCTGACCGTGTCACCATTTTTGGCGAGTCTGCGGGTGGCACGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 56.976; Conservative
                                                     TGTCTTCGCTTGTTGTGTCCCCCATATCCCCAAGGACTCTTCCACGGAGCCATCATGGAGA
                                                                              TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGA
                                                                                                                               TCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="CES2"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                             Mus musculus
                                                                                                                                                    AK033563.1 GI:26329244
                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTG
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 30-0045, Japan (E-mail:genome-res@gsc:riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Please visit our web site for further
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                                /organism="Mus musculus"
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   db_xref="FANTOM_DB:9030624L02"
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/db_xref="GI:26329245"
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/dev_stage="adult"
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/clone="9030624L02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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                                                                               Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institut Physical and Chemical Research (RIKEN), Labbratory for Gene Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, 1 Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URLihttp://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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(ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
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URL:http://fantom.gsc.riken.jp/.
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Please visit our web site for further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; putative similar to CARBOXYLESTERASE PRECURSOR (BC 3.1.1.) (ALI-ESTERASE) (ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (METHYLBUTYRASE) [MESOCTICETUS BUTATUS] (SPTR | 035533, evidence: FASTY, 83%ID, 100%length, match=1677)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYVKADHGDEIFLVFGYQFGNIKLPYTEEEEQLSRRIMKYWANFARHGNPNSEGLPYW
PVMDHDEQYLQLDIQPSVGRALKARRLQFWTKTLPQKIQELKGSQERHKEL"
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LVHVKDTDIAVHTFLGIFFAKFPVGFURFAFFBFBFBFBFBGVTGTSHPNKTLQKNDNLM
GSEDLKMMKLLIPFISMSEDCLYLNIYVPBAHAHEGSNLFWMVWIHGGALTVCGMASMY
GSMLAATEDVVVVAIQYRLGVLGFFSTGDQHAKGNWGYLDQVAALRWVQQNIVHFGGN
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/protein_id="BAC36707.1"
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53. .1732
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'db_xref="taxon:10090"
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       Adachi, J., Aliawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Khira, F., Takaku-Akahira, S., Miramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4927)
6 (bases 1 to 4927)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group
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AK040349

Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A43008BEI2 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (HE-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (MONOBUTYRASE) [Mesocricetus auratus], full insert sequence.
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Mammalia; Eutheria; Rodentia;
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CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Rignary Logical Project of Genome Exploration Research Group in Rignary Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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CTGCCTATGAGGACGTGCTGGTTGTGGTCCAGTACCGGCTAGGAATATTTTGGTTTCT
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(ALI-STERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE
ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
[Mesocricetus auratus] (SPTR | 035533, evidence: FASTY,
70.7%ID, 99.2%length, match=1672)"
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/clone Itb="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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                            Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

CE 6 (bases 1 to 1958)

RS Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Kasukawa, T., Kodoh, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Nishi, K., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito,
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Submitted (16-APR-2002) Yoshihide Hayashizaki,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK078953

Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130231C15 product:similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus], full insert
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Pred. No. 1.3e-92;
0; Mismatches 664;
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prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                            Physical and Chemical Research (RIKEN), Laboratory for Ger Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, PRI:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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ter (GSC)
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/note="unnamed protein product; putative similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus] (SWLSSPROT|Q64419, evidence: FASTY, 78.4%ID, 100%length, match=1674)" cDNA library"

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                                                                                                                                                                                                                  Group Phase I & II Team.
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Please visit our web site for further details.
Please./jenome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                  GTGCCTCCAGAACTC-----AGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCA
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                                                                                                                            TGTGGCTGTTTTCCTGGGAGTCCCCTTTGCCAAGCCCCCTCTTGGCTCCTTGAGATTTGC
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GGGLPHWPEXYQKEGYLKIGASTQAAQRLKDKEVSFWAELFAKESAQRPSHREHVEL"
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/clone_Tib="RIKEN_full-length enriched mouse
/dev_stage="adult"
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp434N0935) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZDD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2888 bp mRNA linear HTC 22-SEP-2004
Homo sapiens mRNA; cDNA DKFZp434N0935 (from clone DKFZp434N0935).
AL713761.
AL713761.1 GI:19584506
                                                                                                                                                                                                                                                                                                                            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434N0935 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (22-SEP-2004) MIPS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_Tib="434 (synonym:
DH10B; sites NotI + SalI"
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          /product="hypothetical protein"
/protein_id="CAD28531.1"
/db_xref="GI:19584507"
                                                             gene="DKFZp434N0935"
codon_start=1
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                                                                                                             'gene="DKFZp434N0935"
                                                                                                                                            note="carboxylesterase 2 isoform
                                                                                                                                                                                                                            clone="DKFZp434N0935"
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|db_xref="RZPD:DKFZp434N0935"
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xref="UniProt/Swiss-Prot:000748"
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STVVANI.SACDQVDSEALVGCLRGKSKEEILAINKPFKMIPGVVDGVFLPRHPQEILA
SADFQPVPSIVGVNNNSEFGMLIPKVMRIYDTOKEMDERASQAALQKMITILMIPFFFG
DILREBYIGHODDPQTIQAQFQEMMADSMFVIP PALQVAHFQCSRAPVFVPSEFQHQPSW
LKNIRPPHMKAHVKFTEEEEQLSRKMKYWAAFARNGVPNGEGIPHWPLFDQEEQYL
QLNIQPAVGRALKAHRLQFWKKALPQKIQELEEPEERHTEL" GQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPBPPBSWSGVRDGTTHPAMCL QDLTAVBSBFLSQFNMTFPSISBMSEDCLYLSITTPAHSHEGSLUPVMVWIHGGALVFG MASLXDGSMLAALENVVVUIQYRLGVESFGDKHAFGNMGYLDQVLAALRWVQOUI AHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPGLIASSADVI /translation="mTaQsrspTTpTfPGpSQRTpLTPCPVQTPRLGKALIHCWTDPGQPLGEQQRVRRQRTETSBPTMRLHRLRARLSAVACGLLLLLVRGQGQDSASPIRTTHT

1246 GGACCACACACACGGGCAGGTGCTGGGGGAGTCTTGTCCATGTGAAGGGCGCCAATGCCG 1305 211 GGAACACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGC Similarity ACTITIGGAGGCAACCCTGACCGTGTCACCATTTTTGGCGAGTCTGCGGGTGGCACGAGTG TCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTTGGCGAGTCCGCGGGAGCCATAAGTG GGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGT 747 TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGG GCATGGCTTCCTTGTATGATGGTTCCATGCTGGCTGCCTTGGAGAACGTGGTGGTGGTCA 1665 GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG TGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTC 1047 AGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCCTGCTGAGGTGCC GTGGCGTGGCCCTCCTGCCCGGCCTCATTGCCAGCTCAGCTGA----TGTCATCTCCA GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC TGTCTTCGCTTGTTGTGTCCCCCATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGA TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGA GCAACTGGGGCTACCTGGACCAAGTGGCTGCACTACGCTGGGTCCAGCAGAATATCGCCC 1785 TCATCCAGTACCGCCTGGGTGTCCTGGGCTTCTTCAGCACTGGAGACAAGCACGCAACCG gereageerecarerrigaregereegeerigeergeerargaggacergerregreg GCCATGAAGGCTCTAACCTGCCGGTGATGGTGGATCCACGGTGGTGCGCTTGTTTTTG CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTG TCCCTTCCGACTCCATGTCTGAGGACTGCCTGTACCTCAGCATCTACACGCCGGCCCATA 1545 ACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACG 507 TGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA---TCAACACATGCTCAAGGTGCATT CACCCCCTGAGCCCCCTGAATCTTGGAGTGGTGAGGGATGGAACCACCCATCCGGCCA 1425 CGANCCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT 390 TGTGTCTACAGGACCTCACCGCAGTGGAGTCAGAGTTTCTTAGCCAGTTCAACATGACCT Conservative 16.0%; Score 345.8; DB 3; Pred. No. 2.9e-82; 0; Mismatches 617; Indels Length 84; Gaps 2019 987 1959 927 1905 867 1845 1725 627 1605 567 1485 447 1365 270 807 687 5

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      Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.
Braunschweig/Germany) within the cDNA sequencing consortium of th
German Genome Project.
                                                                                                                                     Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Osanger, A., Fobo, G., Han, M. and Wiemann, S. The German cDNA Consortium
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3909)
                                                                                                                                                                                                                                                                              Homo sapiens mRNA; cDNA
BX538086
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clone (DKFZp686H0466) is available at the RZPD Deutsches
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m clone DKFZp686H0466).
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Similarity 54.7%;
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Length 3909;

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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686H0466 Further information about the clone and the sequencing project i available at http://mips.gsf.de/projects/cdna/.
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1354 GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG 211 GGAACACCAGGCTGGGATGGATTCAGGGGCAAGCCAAGTCACTGTGCTGGGGAAGCCCTGTGC 270 TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGG GCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGG GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGGATCCACGGTGGTGCGCTTGTTTTTG CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGTTCCCCAGGAGGTGCCTTCAAGACTG TCCCTTCCGACTCCATGTCTGAGGACTGCCTGTACCTCAGCATCTACACGCCGGCCCATA 1593 ACCCGAAATTCGGAGTGTCAGAAGACTGCCTTGCCCTACCTGAACATCTATGCGCCTGCCCACG CACCCCCTGAGCCCCTGAATCTTGGAGTGTGAGGGATGGAACCACCCATCCGGCCA 1473 GCATGGCTTCCTTGTATGATGGTTCCATGCTGGCTGCCTTGGAGAACGTGGTGGTGGTCA TGTGTCTACAGGACCTCACCGCAGTGGAGTCAGAGTTTCTTAGCCAGTTCAACATGACCT TGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA---TCAACACATGCTCAAGGTGCATT CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT 390 GGACCACACACGGGGCAGGTGCTGGGGAGTCTTGTCCATGTGAAGGGCGCCAATGCCG Conservative 0; Score 344.2; DB 3; Pred. No. 8.8e-82; Mismatches 618; Indels 84; Gaps 1653 1533 1413 1353 687 627 567 447 507 S

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    GCCGGGCTCTGAAGGCCCACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCCC 2775
                                             GACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCCC 1746
                                                                                                                                                                                                                                  TGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTC 1635
                                                                                                                                                                                                                                                                                                                                                                           CGCACATGAAGGCAGACCATGTTAA-----
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Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.

Gene expression analysis in response to lung toxicants: I.
Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)

Contact: Shultz MA

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1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 0793

Fax: 530 752 4698
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Average Phred score is 20 or better. All poor quality data
20) and vector/linker sequence has been removed.
High quality sequence stop: 1918.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF111083 CF111083 1918 bp mRNA linear EST 23-JUL-2003 Shultzomica04334 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig3845 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 15.7%; Score 338; DB 7; Length 1918;
Similarity 54.2%; Pred. No. 3.4e-80;
69; Conservative 0; Mismatches 660; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway
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Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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/clone="Contig3845"
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1508 1462	1449 AAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTTGTGTTCGGTGGTGCC
1448 1402	1389 GCTGGTGCACCTGTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACG
1388 1342	1329 TIGCTIGGAGATGITCTITIGIGGICCCTGCACTGATCACAGCTCGATATCACAGAGAT
1328 1282	1269 GCTAATGAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACAGTCTTCTGGAC
1268 1222	1211 TGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTG
1210 1162	1161 CTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCT
1160 1102	1101 APAGCATTTAPAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTG
1100 1042	1041 TTCACTCGAGTGGTTGATGGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAG
1040 982	996AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCT
995 922	960 TCAGACTCTGAGGCCCTGAGGTGCCTGAGGACA
959 862	900 CATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCG
899	840 GGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCC
742	780 TTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAA
682	720 CTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATC
719	660 TTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCT
562	600 GCTGCCTATGAGGACGTGCTGGTTGTTGGTCTCCAGTACCGGCTAGGAATATTTGGTTTC
502	540 IGGTICCCAGGAGGTGCCITCAAGACTGGCTCAGCCTCCATCTITGATGGGTCCGCCCTG
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotatic of 60,770 full-length cDNAs

I Nature 420, 563-573 (2002)

B 6 (bases 1 to 989)

B Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Furuno,M., Hanagaki,T., Hara,A., Hayateu,N., Hiramoto,K., Hiranka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
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                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muzamatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus
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Submitted 'A. Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Subhiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web
                                                                                                                                                                                                                                GATGCTGGTGCACCTGTCTACTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTTGAAGAC
                                                                                                                                                           ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGT
                                                                                                   GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTG
                                                                                                                                                                                                          GATTCTGGTGGACCTGTCTATTTTTATGAGTTTCAGCACAGACCCCATTGCTTTCAAAAC
AGCAGGAAGATGATGAAATACTGGGCTAACTTTGCCAGGAGCGGGGATCCTAACGGTGCC
                              АСССЕДЛАСАТСЯЛЕНТАСТЕССТАССТТТССТСЕЛАСССЕСЛАТССТВАТСЕВЛАС
                                                                                                                                      TCAAGGCCAGCCTTCGTGAAGGCTGACCACACAGACGAAATCCGCTTTCGTTTTTTGGAGGC
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/db_xref="GI:12840657"
/db_xref="GI:12840657"
/translation="MSSMVLFISITCLYVFSSFSVRTSTCLIVFSCFSLRTCNSLAVF
/translation="MSSMVLFISITCLYVFSSFSVRTSTCLIVFSCFSLRTCNSLAVF
SCISLSDLLKSFLMSSTIIMRYAFKSRSRFSGVLVCPGLGEVGVLGSDDDSGGPVYFY
BFQHRPHCFQNSRPAFVKADHTDEIRFVFGGPPLKGDVVMFEBATEEEKLLSRKMXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; putative
serine/threonine kinase 33 (MGD|MGI:2152419,
                                                                                                                                                                                                                                                                                                                                                               WANFARSGDENGADLEPWEVYDENEQYLELDVNISTGRRLKDQRVEFWTDTLELILSA
SKALLSPTFSLILLSLLSPVLLSAAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evidence: BLASTN, 98%, match=367)
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clone_Tib="RIKEN_full-length enriched mouse
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strain="C57BL/6J"
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xref="taxon:10090"
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Pred. No. 3.9e-79;
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2038 bp
Mus musculus, clone IMAGE:5123923,
BC019926
BC019926.1 GI:18044764
                                                                      through the I.M.A.G.E. Consortium/LLNL at: http://i
Series: IRAK Plate: 42 Row: p Column: 20
This clone was selected for full length sequencing
passed the following selection criteria: Similarity
identity to protein
                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I_M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
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clone has the following problem:
Location/Qualifiers
1, 2038
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                      AGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCCTCCAAGGAGCTGCTGACCCT 1021
                                                                                                       AGACATGAAACCATGGCCTGAAGCTCAGAACTTTGCCAATTCTGTGGCCTGTGGCTCTGC
                                                                                                                                                           GCTCTTCCACAGAGCCATATCCCAGAGTGGGATTGTCACGACCATTATGATGG-----A
CAAGCAGAAAACGTGAACATTTCCTACATAGTCAATGACTCCTTCTTCCCACAAAGGCC
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/db_xref="raxon:10090"
/clone="IMAGE:5123923"
/tissue_type="Liver, normal. 5 mc/clone_lib="NCI_CGAP_Li9"
/lab_host="PH10B"
/note="Vector: pCMV-SPORT6"
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                        TTTTTGGACCAGCACCATCCC
                                            ATACTTGGAGATTGGTCTAGAATCACGGACTGGGGTGAAGCTAAAGAAGGGTCGGCTACA
                                                                    GTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGA 1723
                                                                                             CACAGGAAACCCCAATGGCAAGGGGCTGCTTCGTTGGCCCCAATTAAACCAGTTAGAACA
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Search completed: June 15, 2005, 02:39:37 Job time : 7174.54 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Sequence 1, Appli	Sequence 1, Appli	Sequence 3976, Ap	Sequence 8, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 33, Appl	Sequence 16143, A	Sequence 861, App	Sequence 5, Appli	Sequence 6, Appli	Sequence 2516, Ap	Sequence 2515, Ap	Sequence 3, Appli	Sequence 15541, A	Sequence 7, Appli

ALIGNMENTS

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APPLICANT: CARTIES, ROTY A. J.
APPLICANT: Silos-Santiago, Inmaculada
FITTLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
FITTLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
FITTLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
FRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2158
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Best Local Similarity 100.0%;
Matches 2158; Conservative 0,
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ORGANISM: Homo
FEATURE:
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LOCATION: (96)
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US-10-023-515-3 Sequence 3, Application US/10023515 Patent No. 6664091 GENERAL INFORMATION: APPLICANT: Curtis, Rory A. J. APPLICANT: Silos-Santiago, Inmaculada ITILE OF INVENTION: 5310, A NOVEL HUMAN CARBOXYLESTERASE ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/023,515 CURRENT FILING DATE: 2001-12-18 PRIOR FILING DATE: 2001-12-18 PRIOR APPLICATION NUMBER: 60/256,369 PRIOR PRILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 4.0	Oy 2041 CAAGAFTTCTTCAATAAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATAATGGTTT 2100 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 1861 TITGGTTTCCCTTCTCCCCCCATAATTTCTCCCCCCAATCATTAGCTTCTTCTGAACCTCA 1920 Qy 1921 GCTGCTTTCTATGGGGATCCTTGCAAAACAACCAGCTGCTTTCGGATATTTTATGGACTTA 1980 I	 	Qy 1381 ACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTG 1440

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                    GCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACA
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Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
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CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 155
LENGTH: 965
TYPE: DNA
ORGANISM: Homo Bapiens
FEATURE:
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Ghosh, Redoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Ac
FILE REFERENCE: 803
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Pred. No. 1.8e-141;
0; Mismatches 4;
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RESULT 4

US-09-949-016-3799

Sequence 3799, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF PILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 50/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASTEEQ for Windows Version 4.0

LENGTH: 2117
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-4-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARR: FRSESEQ for Windows Version 4.0

SEQ ID NO 555

LENGTH: 2169
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56:
Matches 876; Conservative
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 1.2e-110;
0; Mismatches 639;
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APPLICANT: Danks, Mary K.

APPLICANT: Potter, Philip M.

APPLICANT: Houghton, Peter J.

TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells

FILE REFERENCE: SJ-005
CURRENT APPLICATION UMMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
                                                                                                                                                                                                                                             RESULT 6
US-09-595-682B-27
; Sequence 27, Application
; Patent No. 6800483
; GENERAL INFORMATION:
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                                                                                                                                              and Methods
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; PRIOR APPLICATION NUMBER: PCT/US99/03171
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 2191
; TYPE: DNA
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Pred. No. 1.2e-110;
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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR PILLING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Ruff, Thomas G.

APPLICANT: Ruff, Thomas G.

IITLE OF INVENTION: Engineering plant Resistance to Pyri
IITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1701
TYPE: DNA
ORGANISM: Rabbit
US-09-264-737-3
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US-09-264-737-3
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GENERAL INFORMATION:
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Patent No. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                                                                           Query Match
Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)...(168971)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Human
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Local Similarity 100.0%; Pred. No. 3.7e-40;
1es 176; Conservative 0; Mismatches 0; Indels 0;
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                                                                   CGCGGGTGGATTTTTGGAC 1732
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US-09-810-861B-3
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FILE REFERENCE: BTI-45
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 3, Application US/09810861B
Patent No. 6770799
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Best Local
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APPLICANT: Soreq, Hermona
APPLICANT: Arntzen, Charles J.
APPLICANT: Mason, Hugh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
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ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC 725
                                   GAGAGGACTGTGCTGGTGCCATGAACTACCGGGTGGGAGCCTTTGGCTTCCTGGCCCTG
                                                                                                           GGCTTCTACAGTGGGGCCTCCTCCTTGGACGTGTACGATGGCCGCTTCTTGGTACAGGCC 1353
                                                                                                                                        GCCTTCAAGACTGGCTCAGCCTC-----CATCTTTGATGGGTCCGCCCTGGCTGCCTAT
                                                                                                                                                                                                                 GCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGT 554
                                                                                                                                                                                                                                                              ACCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGACTGCCTGTACCTCAACGTGTGG 1236
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                                                                                                                                                                                   ACACCATACCCCCGGCCTACATCCCCCA---CCCCTGTCCTCGTCTGGATCTATGGGGGT 1293
                                                                                                                                                                                                                                                                                               CTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTAT 494
                                                                                                                                                                                                                                                                                                                                      ACAACCTTCCAGAGTGTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGC 1176
                                                                                                                                                                                                                                                                                                                                                                         ACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATG
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ilarity 51.8%;
Conservative
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Pred. No. 2.6e-30;
0; Mismatches 374;
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APPLICANT: ATTIZEN, Charles J.
APPLICANT: MASOL, Hugh S.
ITILE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
ITILE OF INVENTION: TRANSGENIC PLANTS
ITILE OF INVENTION: TRANSGENIC PLANTS
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT APPLICATION NUMBER: 60/190,440
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4
LENGTH: 14446
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US-09-810-861B-4
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Patent No. 6770799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
FEATURE: misc_feature
LOCATION: (11862)..(12157)
OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
OTHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 u
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             ACAACCTTCCAGAGTGTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGC 480
                                                                                      GGACCCCGTCGCTTTCTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCT
                                                                                                                  GGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCC
                                                                                                                                                                 CCCGGGGGCCCTGTCTCT----GCTTTCCTGGGCATCCCCTTTGCGGAGCCACCCATG
                                                                                                                                                                                                                                        GATGCAGAGCTGCTGGTGACGGTGCGTGGGGGCCCGGCTGCGGGGCATTCGCCTGAAGACC
                                                   ACCTCCTACCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATG
                                                                                                                                                                                                                                                                                                                                                  TTTTTCCTGATTCTCCAGCCCCTGTTGGGACACAGACAGTGGGGAAAAACTGGGCCTTCT 194
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Arntzen, Charles J.
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APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
APPLICANT: Arntzen, Charles J.
APPLICANT: Mason, Hugh S.
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
TITLE OF INVENTION: TRANSGENIC PLANTS
FILE REFERENCE: BTI-45
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOFTMARE: Patentin Ver. 3.1
SEQ ID NO 5
LENGTH: 1725
TYPER: NNA
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US-09-810-861B-5
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                                                                                                                                                           Matches 341;
                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09810861B Patent No. 6770799
                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: human acetylcholinesterase gene optimized for OTHER INFORMATION: expression in plants
                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                           Local Similarity
                                 330 АСGAAССССАССТВСАТССССТССВАТААСТТССВАСААСССССТАСССТААТ 389
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CTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCTACAACCTTCCAGAGT
                                                                                                CCTGTGAACGTGTTCCTCGGAGTCCCCTTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTT 329
                                                                      CCTGTCTCTGCTTTCCTGGGCATCCCCTTTTGCGGAGCCACCCATGGGACCCCGTCGCTTT
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                                                                                                                                                                       6.5%;
                                                                                                                                                 Score 139.4; DB 4;
Pred. No. 1.2e-30;
0; Mismatches 266;
                                                                                                                                                 Indels 12;
                                                                                                                                                                                     Length 1725;
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RESULT 13
US-07-732-962A-1
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                                                                                                                                              MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,962A
FILING DATE: 19910722
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39304/JPW/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Fischer, Meir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: John P. Whit
STREET: 30 Rockefeller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
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PCT-US92-06106-1
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US-07-732-962A-1
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                                                                                                                                                                               Sequence 1, Application PC/TUS9206106
GENERAL INFORMATION:
APPLICANT: Pischer, Meir
TITLE OF INVENTION: ENGYMATICALLY
TITLE OF INVENTION: ACETYLCHOLINE
NUMBER OF SEQUENCES: 2
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Matches
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ge
FEATURE:
NAME/KEY: CDS
                                                                                                                                                       CORRESPONDENCE ADDRESS
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
                                                                                                        STREET:
                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       772
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30 Rockefeller
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Pred. No. 1.3e-30;
0; Mismatches 266
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
TYPE: NUCLEIC ACID
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Best Local (
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06106
FILING DATE: 19920722
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39304-B-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPHONE: (212) 977-9550
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TOPOLOGY: linear
TOPOLOGY: DNA (genomic)
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Similarity 55.1%;
41; Conservative
GCCTCGGTGGGCATGCACCTGCTGTCCCCGGCCCAGCCGGGCCTGTTCCACAGGGCCGTG
                     ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTTCCACAAAGCCATC
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PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PELICATION NUMBER: 2000-09-08
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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RESULT 1 ABB79537 ID ABB7 XX ABB7 XX ABB7 XX ABB7 XX ABB7 XX ABB7 XX Huma XX Carb KW Carb KW diag XX Homo XX H Region Protein Homo sapiens. diagnosis; therapy. Human carboxylesterase family member 53010 23-SEP-2002 ABB79537 standard; protein; WO200250256-A2 Active-site Domain Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory; ABB79537; Peptide (first entry) /note= "p 219. .234 Location/Qualifiers note= label= Mature_protein label= Signal_peptide .545 . 135 "carboxylesterase "predicted carboxylesterase type-B serine active "predicted carboxylesterase type-B signature" 581 B domain"

18-DEC-2001; 2001WO-US049075.

27-JUN-2002.

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US-10-023-515-1 (1-2158) x ABB79537
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28-MAR-2001; 2001US-0279508P.
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       TTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACA
                                   CCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAACTTTGTGC
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The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological
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                                                                                                       Claim
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KW nootropic; neuroprotective; immunosuppressive; haemostatic;
WW antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
Cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; Parkinson's disease;
Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW haematological disease; metabolic disease; sperm dysfunction;
KW haematological disease; metabolic disease; sperm dysfunction;
KW hyroid disorder; hypothyroidism; brain damage; colitis;
Come photo- transduction deficiency; neurological disease; stroke;
W angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
CW draches; thymus; lymph node; muscular system; obesity; anorexia;
CW growth abnormality; precocious puberty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2000; 2000US-0256710P.
20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0266492P.
30-JAN-2001; 2001US-0266492P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-028535P.
08-MAY-2001; 2001US-0289622P.
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SMITHKLINE BEECHAM
GLAXO GROUP LTD.
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Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder disorder

Agarwal P, Martensen (

SA,

Birkeland M, A, Rizvi SK,

Cogswell JP, Kabnick KF, Smith RF, Strum JC, Xie

Ö

2002-508784/54. DB; ABQ86169.

Claim 1(a); Page 312-313; 335pp; English.

The invention relates to an isolated polypeptide with signal sequences countries and in the polypeptides of the invention may be described as, or encorated. The cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, cardiant, antiulcer, virucide, antithyroid, carebroprotective, anorectic, cardiant, antiulcer, virucide, antithyroid. carebroprotective, anorectic, cardiant, antiulcer, or as a vaccine in the prevention of, cancer, cardind healing disorders, infection, atherosclerosis, Parkinson's disease inflammation, neoplastic diseases, nervous system related disorders, and cardiovascular disorders, pancreatitis, respiratory disorders, and cardiovascular disorders, pancreatitis, respiratory disorder, paper immunity, cardiovascular diseases, metrone disease, hyper-immunity, cardiovascular diseases, metrone disease, hyper-immunity, cardiovascular diseases, metrone antitis, cone photo-transduction deficiency, neurological diseases, sparm dysfunction, thyroid disorders e.g. hypothyroidiam, brain damages, colitis, cone photo-

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ABP61004

standard;

protein; 575

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| TrpAlaIleTrpValLeuAlaAlaPro-----
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Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasi
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CC The invention relates to an isolated human drug metabolising enzyme (DME)
CC and its nucleotide. DME is useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of DME, where the disorders
CC are selected from autoimmune/inflammatory disorder such as acquired
CC immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
CC cirrhosis, hepatitis, and cancer; a neurological disorder such as
CC Alrheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC alevelopmental disorder such as renal tubular acidosis, epilepsy,
CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections
CC is an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic
CC disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal
CC disorder such as cystic fibrosis, diabetes and sorders. DME is
CC useful in a number of drug screening techniques and to analyse the
CC proteome of a tissue or cell type. The invention is useful for creating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention or neurological,
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Lee EA, Ding L,
Lal PG, Warren
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15-DEC-2000; 2000US-0256189P.
21-DEC-2000; 2000US-0257713P.
19-JAN-2001; 2001US-02567906P.
02-FEB-2001; 2001US-0266020P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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DB; AAD40574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human drug metabolizing polypeptide, useful in diagnosis, ntion or treatment of autoimmune/inflammatory, cell proliferative, logical, developmental, endocrine, metabolic and gastrointestinal
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g J, Walia NK, Nguyen P
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                                                                  TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC
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                                                                                                                                                                                                                                                                                                                                                                                     Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorders, developmental disorder, endocrine CC disorder, neurological disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the CC invention. Note: The sequence data for this patent is not represented in CC the printed specification, but was obtained in electronic format directly CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtor Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gi Patury S, Shi X, Suarez CJ;
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N-PSDB; ACN42766.
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                                 GATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTGCTTTTGAAGAC
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Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; KW nootropic; neuroprotective; immunosuppressive; haemostatic; KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid; KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid; KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; KW wound healing disorders; atherosclerosis; parkinson's disease; KW while and the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the strong of the stro
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cyrostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, cc neuroprotective, immunosuppressive, haemostatic, antiinflammatory, cc cardiant, antiulcer, virucide, antityroid, cerebroprotective, anorectic, cc and metabolic. Polypeptides and polynucleotides of the invention are cuseful in the treatment, or as a vaccine in the prevention of, cancer, cc wound healing disorders, infection, atherosclerosis, Parkinson's disease cc and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, ciflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, cc hyperproliferation, systemic autoimmune disease, hyper-immunity, cd developmental abnormality, gastrointestinal ulceration, curopathy, cd disorders e.g. hypothyroidism, brain damages, colitis, cone photoctranduction deficiency, neurological diseases, sperm dysfunction, thyroid covulation disorders, diseases in the spinal cord, thyroid gland, heart, cc growth abnormalities, and alleviation of precocious puberty. The cc sequences given in records ABP60965-ABP61019 represent novel human cc proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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                        ATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCA
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ACC ADA5
XX Cytc
XX Cytc
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XW Gene
XW infl
XX IP-W
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                                                                                                                                                                                                           The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                        Claim
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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24-JAN-2002;
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; 2001US-0281136P.
; 2001US-0281863P.
; 2001US-0281906P.
; 2001US-0282020P.
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25-APR-2001;
25-APR-2001;
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29-MAY-2001;
29-MAY-2001;
19-JUN-2001;
19-JUN-2001;
19-JUN-2001;
119-JUN-2001;
12-SEP-2001;
12-SEP-2001;
12-SEP-2001;
13-SEP-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
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03-JAN-2002;
16-JAN-2002;
02-APR-2002;
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2001US-0284234P.
2001US-0285325P.
2001US-0285381P.
2001US-0285381P.
2001US-0285890P.
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2001US-029852P.
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Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD
Gorman L, Shenoy Spena CEA, Smithson G, Burgess CE, Gerla
Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ,
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman <u>~</u> Spytek KA; et CAM, Zerhusen BD; Gerlach ¥.

N-PSDB; WPI; 2003-046858/04.)B; ABX72267.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 1, Page 303; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polypurcleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, articles, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subsortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides invention

Sequence 581

Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
94.31%	95.07%	2597.50	8.96e-244	
Mismatches:	Conservative:	Matches:	Length:	
17	4.	497	581	

Query DB:

Match:

67

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US-10-023-515-1 (1-2158)

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GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAGGGTTA
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06-OCT-2000;
20-OCT-2000;
09-NOV-2000;
16-NOV-2000;
22-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                               drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder inflammatory disorder; endocrine disorder; eye disorder; endocrine disorder; eye disorder; enzyme; gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
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2000US-0238864P.
2000US-0242323P.
2000US-0247581P.
2000US-0247519P.
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2000US-0252837P.
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Ping HZ, L
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t VS, Gandhi AR, C
Lee EA, Lu DAM,
IZ, Sanjanwala MS,
RT, Warren BA, Xu
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Griffin JA, Hafalia AJA, Ison CH, KI
Nguyen DB, Arvizu C, Policky JL, Ra
Tang YT, Tribouley CM, Narinder WK;
u Y, Yang J, Yao MG, Yue H;
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                                       ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGT
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The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide CC peptide of the polynucleotide by contacting the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC with the antibody of the encoded protein, and observing the binding CC sequence the two, a transformant carrying the polynucleotide in an CC expressible manner and an antisense polynucleotide. The oligonucleotide genessible manner for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The oligonucleotide CC genes may be included in them, for developing a diagnostic marker or compression are useful as pharmaceutical agents and many disease-related CC genes may be included in them, for developing a diagnostic marker or compression. The genes are involved in tissue and/or cell considered the polynucleotide in a targets of gene therapy. The genes are involved in tissue and/or cell transcription-related proteins, signal transduction-related proteins, conservation, and activity, or as targets conservation, diseases (e.g. osteoporosis, conservation) and cativity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed consequence data for this patent is not represented in the printed consequence information supplied by the
                  Alignment Scores:
Pred. No.:
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ADB64065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001; 2001JP-00379298
25-JAN-2002; 2002US-00350978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related prot transcription-related protein; osteoporosis; neurological disease;
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Yoshikawa T,
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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 GGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAG
                                                                                                                                               GCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCT
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                                                                                                                                AlaLeuHisLeuIleGinAsnileLeuHisIleProProGinTyrLeuHisLeuValAla
                        LeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHisArgAspAla
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The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosing cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin
                                                                                                                                                                                                                                Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
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                                                     GlyAspGluArgLysLysAspLeuGlnValLeuAlaArgIleCysGlyCysHisAlaSer
                                                                        GATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCA
                                                                                                                                                      TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTG----GAGGCCCAT
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                                             04-MAR-2002; 2002JP-00057908
                                                                                      04-MAR-2002; 2002JP-00057908
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TOHOKU TECHNOARCH KK
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The present sequence represents a cat cauxin protein (I) or its salt, CC which is cat kidney disease marker. Also described: (1) a partial peptide CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (III); (3) a vector CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or CC (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) CC disease which involves measuring (I) quantitatively, and where reduction CC of amount of (I) indicates presence of the disease; (8) a cat kidney CC disease diagnostic agent comprising (I) labelling agent, a reagent which CC describe the biological activity of urinary (I) or (VI); and (9) a cauxin CC detection kit which measures cauxin in a test sample. (I) is useful as a CC disease. (I) enables detection of cat kidney disease simply and correctly. (I) provides an early marker for the disease, and replaces CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
                                        blood testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel cauxin protein or its salt, useful as a cat kidney disease marker, and for diagnosing cat kidney disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-002277/01.
DB; ADF50146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO
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Best Local Si
Query Match:
DB:
                  Percent Similarity:
Best Local Similarity:
                                           Alignment Scores:
Pred. No.:
 5.58e-184
1985.00
83.27%
71.73%
51.27%
       Conservative: Mismatches: Indels:
                               Length:
Matches:
542
373
85
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US-10-023-515-1 (1-2158) x ADF50147 (1-542)

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ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                                           CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
                                                                                                                                                               GinHisValLeuLysValArgTyrProLysLeuGluAlaSerGluAspCysLeuTyrLeu
                                      TyrGluAspValLeuIleValThrThrGlnTyrArgLeuGlyIlePheGlyPhePheAsp
                                                   TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
                                                                                ProGlyGlyAlaPheLysMetGlySerAlaSerSerPheAspGlySerAlaLeuAlaAla
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                                                                                                      GluGlyValProLeuTrpProAlaTyrThrGlnSerGluGlnTyrLeuLysLeuAspLeu
                                                                                                                    AACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTG
                                                                                                                                                                CTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
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                                                        serValSerValGlyGlnLysLeuLysGluGlnGluValGluPheTrpMetAsnThrIle
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wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; trachea; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
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27-JUN-2002.

17-DEC-2001; 2001WO-US049232

19-DEC-2000; 20-DEC-2000; 09-JAN-2001; 30-JAN-2001;

06-FEB-2001; 19-MAR-2001; 04-APR-2001; 08-MAY-2001; 2000US-0257048P. 2001US-0260482P. 2001US-0264922P. 2001US-0266797P. 2001US-0266797P. 2001US-0276988P. 2001US-0281535P. 2001US-0281535P.

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Martensen Agarwal ָּט SA, Birkeland BA, Rizvi S Cogswell JP, Kabnic Smith RF, Strum JC, Kabnick KF, rum JC, Xie Ö K

WPI; 2002-508784/54.)B; ABQ86171.

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder

Claim 1(a); Page 315; 335pp; English.

The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cCC cycostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, cCC neuroprotective, immunosuppressive, haemostatic, antinflammatory, cCC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polymucleotides of the invention are cueful in the treatment, or as a vaccine in the prevention of, cancer, cCC wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, cCC hyperproliferation, systemic autoimmune disease, hyper-immunity, cardiovascular diseases, mervous system related disorders, cCC hyperproliferation, systemic autoimmune disease, hyper-immunity, cardiovascular diseases, mervous system related disorders, cCC haematological diseases, mervous system related disorders, cCC haematological diseases, mervous system related, thyroid developmental abnormality, gastrointestinal ulceration, neuropathy, cardiovascular, et abolic diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photoctransduction deficiency, neurological diseases, stroke, angiogenesis,

ABP61006

standard;

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                                                                         AspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGlu
                                     GlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyz
                                                                                     GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAA 1538
                                                                                                              ArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAla
                                                                                                                          GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT
                                                                                                                                                    CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT
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                                                                                                                                                                                         LeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValValPro
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                                                                                                                                                                                                                                                                                                                                                        GGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATT 1118
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RESULT 14
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XX Rat;
KW Rat;
KW Osteo
KW dectox
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cancer and osteoporosis. are useful Novel human n carboxylesterase-like enzyme polypeptide, regulators of which for preventing and treating organophosphorus intoxication,

WPI; 2002-195808/25.

(FARB)

BAYER

Disclosure; Fig 8; 92pp; English.

The invention relates to a purified human carboxylesterase-like enzyme CC polypeptide. Carboxylesterase-like enzyme and its DNA are useful for CC screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is useful for treating a carboxylesterase-like enzyme discompounds that increase the ability of human carboxylesterase-like enzyme compounds that increase the ability of human carboxylesterase-like enzyme compounds are useful as detoxifying agents. CC carboxylesterase-like enzyme agonists and antagonists are useful for creating osteoporosis, Paget's disease and degradation of bone implants, CC diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of coding sequence of carboxylesterase-like enzyme before coding sequence of carboxylesterase-like enzyme polymucleotide is useful in gene therapy and for generating antisense oligonucleotides or carboxylesterase-like enzyme polymucleotides or carboxylesterase-like enzyme polymucleotides or carboxylesterase-like enzyme polymucleotides are useful for modulating carboxylesterase-like enzyme gene expression. The present sequence is rat carboxylesterase-like enzyme gene expression. The present sequence is rat carboxylesterase-like enzyme protein

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                      CTGAGGTGCCTGAGGACAAAACCCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAAACAAAG
                                                              GACCTGCAG----GTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB59171 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nontropic; antinflammatory; antiulcer; vulneray; anticonvulsant; antidabetic; antifulgal; antiparastic and cardiant activity. The polynucleotide and CC antifungal; antiparastic and cardiant activity. The polynucleotide and CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists of immune disorders e.g. Addison's diagnosis, prevantion and treatment CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colhris; cardiovascular disorders such as myocardial ischaemias; wound healing; infarriance disorders such as cerebral anoxia and epilepsy; and
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-UNITS=5bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_M10= -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
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thiolesterase B (EC 3.-.-.) precursor - mallard C;Species: Anas platyrhynchos (mallard) C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_C;Accession: A47162 R;Hwang, C.S.; Kolattukudy, P.E. J. Biol. Chem. 268, 14278-14284, 1993 A;Reference number: A47162; MUID:93300823; PMID:8314791 A;Accession: A47162. Ś 밁 S Percent Similarity:
Best Local Similarity:
Query Match: A;Cross-references: UNIPROT:Q04791; GB:L05493; NID:g213100; PIDN:AAA49223.1; PID:g213101 C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: hydrolase 밁 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-557 <HWA> US-10-023-515-1 (1-2158) x A47162 (1-557) Score: Pred. No.: Alignment Scores: F;56-545/Domain: cholinesterase homology <CHE> 243 CAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCT 302 303 GCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAAC 362 43 GinvalLysvalAsnAlaAlaGluArgSerValAsnValPheLeuGlyLeuProPheAla 23 ThrGlyGlnLysAlaGluGlnProGluValValThrAsnTyrGlySerValArgGlyTyr 42 7.1e-91 1298.50 62.77% 48.36% 33.54% Length: Matches: 05-May-1995 #text_change 09-Jul-2004 Gaps: Mismatches: Indels: Conservative: 557 265 79 177 27 œ CDNA and stimulation of expre 62

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60K esterase (BC 3.1.1.-) isoform 2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990
C;Accession: A34329
R;Ozols, J.
R;Ozols, J.
Cham 264 12533-12545, 1989
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A/Cross references: UNIPROT:P14943
C;Superfamily: cholinesterase; cholinesterase home
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
C;Keywords: cholinesterase homology <CHE>
F;32-517/Domain: cholinesterase homology <CHE>
F;201,430/Active site: Ser, His #status predicted
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A;Molecule type: protein
A;Residues: 1-532 <OZO>
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A;Title: Isolation,
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ProAlaMetCysLeuGlnAsn---
                                                                                GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT 1418
                                                                                                                                                       CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT 1358
                                                                                                                                                                                                                       CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC
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                                                                                                                                                                                     ----ProProAlaLeuGlyAspLeuLeuMetAspGluTyrMetGlySerAsnGluAsp
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                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Reywords: carboxylic ester hydrolase; glycoprotein F;58-544/Domain: cholinesterase homology <CHE> F;15-95,123-280,291-428/Disulfide bonds: #status predicted F;111,276/Binding site: carbohydrate (Asn) (covalent) #status F;228,457/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carboxylesterase (EC 3.1.1.1) - human (;Species: Homo sapiens (man) (;Cpate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 (;Accession: JC5408 R;Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G. Biochem. Biophys. Res. Commun. 233, 117-120, 1997 A;Title: Molecular cloning and characterization of a novel putative carboxylesterase, A;Reference number: JC5408; MUID:97289502; PMID:9144407 A;Accession: JC5408; MUID:97289502; PMID:9144407 A;Accession: JC5408.
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A;Experimental source: intestine
C;Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters &
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C;Superfamily: cholinesterase; cholinesterase homology
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A; Residues: 1-559 <SCH>
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                                                                                                                                                                                                       26 GlyGlnAspSerAlaSerProIleArgThrThrHisThrGlyGlnValLeuGlySerLeu
                     CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC-----
 ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu 105
                                                                   CCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 365
                                                                                                                                     ValHisValLysGlyAlaAsnAlaGlyValGlnThrPheLeuGlyIleProPheAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaArgAsnArgAsnProAsnGlyGluGlyLeuAlaHisTrpProLeuPheAspLeuAsp 487
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1230.00
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                                                     IleProAlaLeuGlnValAlaHisPhe---GlnCysSerArgAlaProValTyrPheTyr
                                                                    GTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTAT
                                                                                                          GlyAspProGlnThrLeuGlnAlaGlnPheGlnGluMetMetAlaAspSerMetPheval
                                                                                                                                  ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG
                                                                                                                                                                                                                AspThrGlnLysGluMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr 377
                                                                                                                                                                                                                                                                                                                                                                                                   AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT 1064
                                                                                                                                                            LeuLeuMetLeuProProThrPheGlyAspLeuLeuArgGluGluTyrIleGlyAspAsn
                                                                                                                                                                                                                                        GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTTCCATCTGATACAAAAC 1232
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| IleValGlyValAsmAsmAsmCluPheGlyTtpLeuIleProLysValMetArgIleTyr 357
                                                                                                                                                                                                                                                                                            ATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCTG------ATGAAG 1172
                                                                                                                                                                                                                                                                                                                                        GluGluIleLeuAlaIleAsnLysProPheLysMetIleProGlyValValAspGlyVal 317
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|ValMetValTrpIleHisGlyGlyAlaLeuValPheGlyMetAlaSerLeuTyrAspGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-561 <SON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carboxylesterase (EC 3.1.1.1) precursor - golden hamster C; Species: Mesocricetus auratus (golden hamster) C; Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_c; Accession: S47655 R; Sone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y. Biochim. Biophys. Acta 1207, 138-142, 1994 A;Title: Cloning and sequence analysis of a hamster liver A;Reference number: S47655; MUID:94318665; PMID:8043605 A;Accession: S47655
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S47655
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||||||||
|AsnIleTyrThrProAlaHisAlaHisGluGlySerAsnLeuProValMetValTrpIle
                 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGGTCTTGGTGTGGTTC
                                                                                                                                                                                                                                                     CCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 365
                                                                                                                                                                                                                                                                                                ValTyrValLysGluGlyValThrGlyValTyrAlaPheLeuGlyIleProPheAlaLys 65
                                                                                                                                                                                                                                                                                                                                   GICACIGIGCIGGAAGCCCIGIGCCIGIGAACGIGITCCTCGGAGICCCCTTIGCIGCT 305
                                                                      SerLysGluArgLysIleIleLeuProThrIleSerMetSerGluAspCysLeuTyrLeu
                                                                                                           CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
                                                                                                                                             ArgAspGlyThrSerGluProAlaMetCysLeuGlnThrAspPheMetArgProGlnIle 105
                                                                                                                                                                            CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT
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                                                                                                                                                                                                                                                                                                      ProGlnThrLeuGlnAlaGlnPheArgGluLeuMetLysAspPheMetPheValllePro
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GluLeuLeuAlaSerValAspPheHisProValProSerIleIleGlyValAspSerAsp
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SerGluAlaLeuValHisCysLeuArgGluLysThrGluAlaGluIleLeuAlaIleAsn
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                                                                                                                                                                                                                           CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC
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                                 GTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGGTTACTGAGCCGGAAGATGATGAAATAC 1586
                                                                                                                                                                                                                                                                 GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT
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                                                                       HisGlyAspHisValAlaPheValPheGlySerAspPheTrpGlyLeuLysIleAspLeu
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <AID>
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
F;46-535/Domain: cholinesterase homology <CHE>
F;415,443/Active site: Ser, His #status predicted
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S34607
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34607
R;Aida, K.; Moore, R.; Negishi, M.
Biochim. Biophys. Acta 1174, 72-74, 1993
A;Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase
A;Heference number: S34607; MUID:93326638; PMID:7916639
A;Accession: S34607; MUID:93326638; PMID:7916639
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TATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTTGTTGGTTCCCAGGA 551
                                                                                                                                                           ATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATC
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                                                                                                                             ThrieuAsnGluLysMetLysIlePheProIleSerGluAspCysLeuThrLeuAsnIle
                                                                                                                                                                                            AlaSerIleAsnProProMetCysLeuGlnAspValGluArgMetSerAsnSerArgPhe
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         ACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAAT 1652
GlnPheAlaArgThrGlyAsnProAsnGlyLysGlyLeuProProTrpProGlnLeuAsn
                                     SerGluAsnAlaPheValPheGlyGlyProPheLeuThrAspGluSerSerLeuLeuAla
                                                                                         GATGAAGTCCGCTTTGTGTTCGGTGGTCCTTCCTG-----AAGGGGGACATTGTTATG
                                                                                                                  GlnGluAspLeuLeuGluAsnSerArgProLeuLeuAlaHis------Met 364
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-554 <OVN>
A;Coross-references: UNIPROT:P23953; GB:M57960; NID:g192853;
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
F;50-540/Domain: Cholinesterase homology <CHE>
F;221,455/Active site: Ser, His #status predicted
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A39060
carboxylesterase (EC 3.1.1.1) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 09-Jul-2004
C;Accession: A39060
R;Ovnic, M; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, S.G.; Cenomics 9, 344-354, 1991
A;Title: Characterization of a murine cDNA encoding a member of the carboxylesterase |
A;Reference number: A39060; MUID:91169540; PMID:1840565
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                                                                          GlyLeuVallleGlyGlyArgSerProTyrAsnGlyLeuAlaLeuSerAlaHisGluAsn 162
                                                                                                 GCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTTGCCTATGAGGAC
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serProAlaAspLeuThrLysSerSerGlnLeuProValMetValTrp11eHisGlyGly
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ThrGluLysGluIleLeuProLeuLysIleSerGluAspCysLeuTyrLeuAsnIleTyr 122
                                                                                                                                                                                                                                                                                                                      TyrProProMetCysSerGinAspAlaGlyTrpAlaLysIleLeuSerAspMetPheSer 102
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GlnLeuGluGlnTyrLeuGluIleGlyLeuGluProArgThrGlyValLyBLeuLyBLy8 524
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                                                                                                                                    GluGluThrAsnLeuSerLysMetValMetLysPheTrpAlaAsnPheAlaArgAsnGly
                                                                                                                                                            GAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGG
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GlnIleGlyAlaThrThrGlnGlnAlaGlnArgLeuLysAlaGluGluValAlaPheTrp
                                                                                                                                                                                                           PheValPheGlyAlaProLeuLeuLys------GluGlyAlaSerGlu
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A;Rolecule type: protein
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A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: and 33-Leu were also found
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glyc
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: carboxylesterase #status experimental <MAT>
F;51-552/Domain: cholinesterase homology <CHE>
F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222,467/Active site: Ser, His #status predicted
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A;Title: The nucleotide and
A;Reference number: S19307;
A;Accession: S19307
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N;Alternate names: proline-beta-naphthylamidase
C;Species: Sus scrofa domestica (domestic pig)
C;Pate: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Date: 04-Dec-1992 #S2607
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A; Residues: 1-566 < MATI>
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                                CCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGAT 587
                                                                                   GAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC
                                                                                                                                      AspLeuPheThrAsnGlyLysGluArgLeuThrLeuGluPhe-----
                                                                                                                                                                        GAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCA 467
                                                                                                                                                                                                                                             GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC------
                                                                                                                                                                                                                                                                                                CCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGA 368
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SerLeuGluGlyLeuAlaGlnProValAlaValPheLeuGlyValProPheAlaLysPro
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 ProvalMetValTrpIleHisGlyGlyGlyLeuValLeuGlyGlyAlaProMetTyrAsp
                                                                                                                                                                                                         AsnThrThrSerTyrProProMetCysCysGlnAspProValValGluGlnMetThrSer
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Matches:
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SerValPheGlyPheProLeuLeuLysGlyAsp------AlaProGlu
                        GluGluValSerLeuSerLysThrValMetLysPheTrpAlaAsnPheAlaArgSerGly
                                                 GAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGG
                                                                                                     TTTGTGTTCGGTGGTGCCTTCCTGAAGGGGACATTGTTATGTTCGAAGGAGCCACGGAG
                                                                                                                                                        CAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGC 1490
                                                                                                                                                                                                GCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCT
                                                                                                                              SerPheSerSerAspLysLysProLysThrValIleGlyAspHisGlyAspGluIlePhe
                                                                                                                                                                                 AlaArgGlnHisArgAspAlaGlyAlaProThrTyrMetTyrGluPheGlnTyrArgPro
                                                                                                                                                                                                                                    CGAGACAGTCTTCTCGGACTTGCTGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACA 1370
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                                                                                                                                                                                                                                                                                     GluLeuThrProValAlaThrAspLysTyrLeuGlyGlyThrAspAspProValLysLys 412
                                                                                                                                                                                                                                                                                                               AspGlnLysThrAlaThrSerLeuLeuTrpLysSerTyrProIleAlaAsnIleProGlu 392
                                                                                                                                                                                                                                                                                                                                                                                                                      CACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCC---
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A;Molecule type: mRNA
A;Residues: 1-549 <TAK>
A;Residues: 1-549 <TAK>
A;Experimental source: liver
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; microson
F;1-18/Dromain: signal sequence #status predicted <SIG>
F;19-54/Product: carboxylesterase E1 #status predicted <MAT>
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F;79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;221,453/Active site: Ser, His #status predicted
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JX0054
Carboxylesterase (EC 3.1.1.1) E1 precursor, minor form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_chan
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_chan
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_chan
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_chan
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revision 30-Jun-1992 #sequence_revis
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LeuAlaValCysProIleTrpGlyHis-------ProSerSerPro
TGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCCATCTTTGATGGGTCCGCCCTG
                                                                                                                                                                                     TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG
                                                                                                                            TyrLeuAsnIleTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
                                                                                                                                                                                                                                                                                                                                                 TTAGATCAACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCCTAATTTGTGCCTCCAGAAC------
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                                                                                                                                                                                                                                                                                                             ThrGlyLysGluSerIleProLeuGluPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheThrGlnProValAlaValPheLeuGlyValProPheAlaLysProProLeuGlySer 62
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ArgAsnGlyAsnProAsnGlyGluGlyLeuProHisTrpProGluTyrAspGlnLysGlu
                                             GCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 160
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A;Molecule type: mRNA
A;Residues: 61-567 <LON>
A;Residues: 61-567 <LON>
A;Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A;Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A;Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A;Cross-references: GB:M5509; NID:g179929; PIDN:BAA06473
T.
Genomics 17, 76-82, 1993
A;Title: Mn Olecular cloning and characterization of a human carboxylesterase gene.
A;Reference number: A47376; MUID:94010913; PMID:8406473
A;Ccossion: A47376
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecular type: mRNA; DNA
A;Residues: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecular type: mRNA; DNA
A;Residues: 1-3, PALV', 8-11, 'A',13-567 <SHI>
A;Cross-references: GB:D21088; NID:g455476; PIDN:BAA04650.1; PID:g458470
A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correspond
R;Zschunke, P.; Salmassi, A.; Kreipe, H.; Buck, F.; Parwaresch, M.R.; Radzun, H.J.
Blood 78, 506-512, 1991
A;Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase-1
A;Reference number: A49816; MUID:91300111; PMID:2070086
A;Molecule type: mRNA;
A;Residues: 1-55, 'G', 57-361,363-535, 'G', 537-567 <KRO1>
A;Cross-references: GB:L07765; NID:g180949; PIDN:AAA35711.1;
A;Accession: A48809
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A; Residues: 'G', 65-185, 'G', 187-361,363-567 < ZSC>
A; Residues: 'G', 65-185, 'G', 187-361,363-567 < ZSC>
A; Cross-references: GB: X52973; NID: 936421; PIDN: CAA37147.1; PID: 91335304
A; Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A; Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.
A; Reference number: PS0280; MUID: 92084150; PMID: 1748313
A; Accession: PS0280
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Carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human carboxylesterase; carboxylesterase, hepatic; monocyte/macrophage serine esterase (f.Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A41010; JH0327; A47376; A49816; P80280; I61085; A48809; I57004
R;Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J. Biol. Chem. 266, 18832-18838, 1991
A;Title: A serine esterase released by human alveolar macrophages is closely related A;Reference number: A41010; MUID:92011649; PMID:1918003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mrNA
A;Residues: 114, 'H',116-280,'A',282-300,'IGNSYLWTYRETQREST',318-336,'R',338-382,'GSPI',
A;Residues: 114, 'H',116-280,'A',282-300,'IGNSYLWTYRETQREST',318-336,'R',338-382,'GSPI',
A;Rosidues: GB:M65261; NID:g187028; PIDN:AAA83932.1; PID:g187029
A;Experimental source: liver
A;Note: differences between this sequence and other reports appear to be due to framest
A;Note: differences between this sequence and other reports appear to be due to framest
A;Note: differences between this sequence and other reports appear to be due to framest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kroetz, D.L.; McBride, O.W.; Gonzalez, F.J.
Biochemistry 32, 11606-11617, 1993
A;Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxyles
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A; Residues: 1-567 < MUN>
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A;Residues: 1-17,'A',18
A;Cross-references: GB:CGenetics:
A;Gene: GDB:CES1; HMSE
A;Cross-references: GDB:
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C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum;
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-145/Domain: propeptide #status predicted <PRO>
F;19-155/Domain: cholinesterase homology <CHE>
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F;221,468/Active site: Ser, His #status predicted
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GlyGluSerAlaGlyGlyGluSerValSerValLeuValLeuSerProLeuAlaLysAsn
                                                   ArgTrpValGlnAspAsnIleAlaSerPheGlyGlyAsnProGlySerValThrIlePhe
                 GGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGC
                                                                     TCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTT
                                                                                                          SerThrGlyAspGluHisSerArgGlyAsnTrpGlyHisLeuAspGlnValAlaAlaLeu
                                                                                                                             ACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTG
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                                                                                                                                                              AlaHisGluAsnValValValValThrTleGlnTyrArgLeuGlyTleTrpGlyPhePhe
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carboxylesterase (EC 3.1.1.1) ES-4 precurso; N;Alternate names: hydrolase B C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Oct-1996 #sequence_revision 13-Mac;Accession: S62788; S51203; A55304; S49257 R;Robbi. M.; van Schaftingen, E.; Beaufay, I Biochem. J. 313, 821-826, 1996
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A,Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal palmitoy)
A,Reference number: 86788; MUID: 96190723; PMID: 8611161
A,Accession: 802788
A,Accession: 802788
A,Accession: 802788
A,Redicuse: 1-561 -48089
A,Cross-references: UNIFROT: 0646573; EMBL:X81825; NID: 9550417; PIDN:CAA57419.1; PID: 95504
A,Cross-references: UNIFROT: 0646573; EMBL:X81825; NID: 9550417; PIDN:CAA57419.1; PID: 95504
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A,Cross-reference number: 551202; MUID: 95077430; PMID: 798698
A,Accession: 591203
A,Molecula: type: protein
A,Residues: 19-48 -4M02*
A,ACCession: A,E304
A,ACCession: A,E304
A,ACCession: A,E304; MUID: 95050819; PMID: 7981958
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    GATCAACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTAC 482
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ThrAsnArgLysGluLysIleHis-----LeuGluPheSerGluAspCysLeuTyr
                                                                                    AGAGATGCTGGTGCACCTGTCTATGAGTTTTCGGCACCGGCCTCAGTGCTTTGAA
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                                                               ArgAspAlaGlyAlaProThrTyrMetTyrGluTyrGlnTyrTyrProSerPheSerSer 455
                                                                                                                                             LeuAlaPheIleGlyAspValSerPheSerIleProSerValMetValSerArgAspHis
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ProGlnArgProLysHisValValGlyAspHisAlaAspAspLeuTyrSerValPheGly

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RESULT 11

A55281

Carboxylesterase (EC 3.1.1.1) egasyn - mouse

N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-
C;Species: Mus musculus (house mouse)
C;Accession A55281
C;Accession A55281
R;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;
A;Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-
A;Reference number: A55281
A;Reference number: A55281; MUID:92147141; PMID:1783403
A;Residues: Dreliminary
A;Molecule type: mRNA; protein
A;Residues: 1-562 <OVN>
A;Cross-references: UNIPROT:Q64176; GB:S80191; NID:g244727; PIDN:AAB21335.1; PID:g244728
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
F;51-552/Domain: cholinesterase homology <CHE>
F;222,467/Active site: Ser, His #status predicted
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                    TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG
                                                                     CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTG-----TCAGAAGACTGCCTC:::|||
                                                                                                            LysAsnAlaThrSerTyrProProMetCysPheGlnAspProValThrGlyGlnIleVal
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Carboxylesterase (EC 3.1.1.1) precursor - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Cate: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004 C;Accession: A31584 C;Accession: A31584 R;Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R. Biochem. Biophys. Res. Commun. 156, 866-873, 1988 A;Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for A;Reference number: A31584; MUID:89050119; PMID:2973315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-540 <LON>
A; Residues: 1-540 <LON>
A; Residues: 1-540 <LON>
A; Cross-references: UNIPROT: P10959; GB: M20629; GB: X13587; NID: g203279; PIDN: A
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase; glycoprotein
F; 1-9/Domain: signal sequence #status predicted <SIG>
F; 10-540/Product: carboxylesterase #status predicted <MAT>
F; 41-529/Domain: cholinesterase homology <CHE>
F; 41-529/Domain: cholinesterase homology <CHE>
F; 70, 265, 266, 293, 366, 467/Binding ster: carbohydrate (Asn) (covalent) #status
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                                                                              GCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 1601
                                                                                                             GluIlePheSerValPheGlyThrProPheLeuLys-----GluGly
                                                                                                                                                                        CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGAT 1481
                                                                                                                                                                                                                                    ACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCA 1361
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R;Yan, B.; Yang, D.; Parkinson, A.
Arch. Biochem. Biophys. 317, 222-234, 1995
A;Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase fam A;Reference number: S71597; MUID:95177656; PMID:7872788
A;Reference number: S71597 MUID:95177656; PMID:7872788
A;Reference number: S71597 MUID:95177656; PMID:7872788
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A;Reference number: S01597; MUID:95177656; PMID:78727288
A;Reference number: S01597; MUID:951766; PMID:78727288
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                                                                                 GACTGCCTCTACCTGAACATCTATGCGCCCTGCCCACGCCGATACAGGCTCCAAGCTCCCC
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                                                             AspCysLeuTyrLeuAsnIleTyrThrProAlaAspPheThrLysAspSerArgMetPro
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GAGGAGAAGTTACTGAGCCGGAAGATGATGATAATACTGGGCTACCTTTGCTCGAACCGGG
                                                                                                      TTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAG
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                                                                      ServalPheGlyAlaProIleLeuArg-----
                                                                                                                                     SerPheSerSerProGlnArgProLysAspValValGlyAspHisAlaAspAspValTyr
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                                                                                                                                                                                                            SerArgAspHisArgAspAlaGlyAlaFroThrTyrValTyrGluTyrGlnTyrTyrPro
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 503-554,'R', 556-561 <MED>
A;Cross-references: EMBL:X65295; NID:g57557; PIDN:CAA46390.1;
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: edicatoraylic seter hydrolase; glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-561/Product: carboxylesterase ES-3 #status predicted <MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Jate: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004 C;Accession: JC2447; S23462 R;Robbi, M.; Beaufay, H. Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994 Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994 A;Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN). A;Reference number: JC2447; MUID:95032008; PMID:7945287 A;A;Cession: JC2447; MUID:95032008; PMID:7945287
                                                                                                                                                                                                                                                                                                                                                                                                                                             F;50-551/Domain: cholinesterase homology <CHE>
F;79,107,489/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;221,466/Active site: Ser, His #status predicted
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R;Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
Eur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal sequence
A;Reference number: S23460; MUID:92299008; PMID:1606962
A;Accession: S23462
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A;Residues: 1-561 <ROB>
A;Cross-references: UNIPROT:Q63108; GB:X81395; NID:g550146; PIDN:CAA57158.1; PID:g55014
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                                                                                                                                                     CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC 1298
                                                                                                                                                                                                                CTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC-----ATCCTG 1238
                                                                                                                                                                                                                                               GGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT---ATGAAGGAGGCTCCTGAGATC 1187
                                                                                                                                                                                                                                                                                                           ProLysMetProGluGluIleLeuAlaGluLysAspPheAsnThrValProTyrIleVal
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                                                                                                                       AsnLeuProGluGluAlaIleProValAlaValGluLysTyrLeuArgHisThrAspAsp
                                                                                                                                                                                     AspMetLysLeuAspProMetThrAlaThrSerLeuLeuLysLysSerSerPheLeuLeu
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A;Molecule type: mRNA

A;Residues: 1-264,'K',266-565 <ROB2>
A;Cross-references: EMBL:X51974; NID:956898; PIDN:CAA36236.1; PID:956899

R;Morgan, E, W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.

A;Title: Purification and characterization of two rat liver microsomal carbo:
A;Reference number: S51202; MUID:95077430; PMID:7986098

A;Accession: S51202

A;Molecule type: protein
A;Residues: 19-48 <MOR>
R;Medda, S.; Prota, R.L.

Eur. J. Biochem. 206, 801-806, 1992

A;Ritle: The carboxylesterase family exhibits C-terminal sequence diversity ra;Reference number: S23460; MUID:92299008; PMID:1606962

A;Accession: S23460

A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxylesterase (EC 3.1.1.) ES-10 precursor, microsomal - rat N;Alternate names: hydrolase A C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-C;Accession: S10367; S12468; S51202; S23460; S14361 R;Robbi, M; Beaufay, H.; Octave, J.N.

Biochem. J. 269, 451-458, 1990 A;Fitle: Nucleotide sequence of CDNA coding for rat liver pI 6.1 es A;Reference number: S10367; MUID:90351366; PMID:2386485 A;Robeicus: S10367 A;MOID:90351366; PMID:2386485 A;Rocession: S10367 A;Robbi, M. 1-565 - ROBIL
A;Cross-references: UNIPROT:09R135; EMBL:X51974 A;Note: 168-G1n, 247-Lys, 423-Met, and 506-Asn were also found A;Note: the sequence from Fig. 4 is inconsistent with that from Fig.
                                          A;Molecule type: mRNA
A;Residues: 1-185,'(7,187-422,'M',424-505,'N',507-565 <MED>
A;Residues: 1-185,'(7,187-422,'M',424-505,'N',507-565 <MED>
A;Cross-references: EMBL:X65296; NID:g57553; PIDN:CAA46391.1;
A;Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Blochem. J. 274, 693-697, 1991
A;Title: purification and characterization of carboxylesterase
A;Reference number: S14361; MUID:91190080; PMID:2012599
A;Accession: S14361
   A;Molecule type: protein
A;Residues: 19-26,'D',28-37 <GAU>
,C;Superfamily: cholinesterase; ch
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PMID:2012599
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AlaLeuIleThrThrAspSerLysProIleAlaAsnLeu-----IleAlaThrLeuSer
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C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; F;1-18/Domain: signal sequence #status predicted <SIG>F;19-565/Product: carboxylesterase #status predicted <MAT>F;50-551/Domain: cholinesterase homology <CHBS
F;79,489/Binding site: carbohydrate (Asn) (covalent) #status predicted
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TACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGT
                                                                         CCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCT
                                                                                                                                                                                   GinValAlaAlaLeuHisTrpValGinAspAsnileAlaAsnPheGiyGiyAsnProGly
                                     ProLeuAlaLysAsnLeuPheHisArgAlaIleSerGluSerGlyValValLeuThrSer
                                                                                                               SerValThrilePheGlyGluSerAlaGlyGlyPheSerValSerAlaLeuValLeuSer
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372 AspGlnLysThrAlaLysSerLeu---LeuTrpLysSerTyrProThrLeuLysIleSer 390
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TrpSerGlu------LeuArgAlaLysGluAlaAlaGluGluPro 557
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|GlySerProAsmGlyGlyGlyLeuProHisTrpProGluTyrAspGlnLysGluGlyTyr 524
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                                                                                                                                  TGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCT 1781
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Search completed: June 15, 2005, 08:55:12 Job time : 72.97 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Result
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-MODEL=frame+ n2p.model -DEV=xlh
-Q=/Cgn2 1/USPTO_Spool/664091/runat_14062005_133459_9335/app_query.fasta_1.4238
-Q=/Cgn2 1/USPTO_Spool/664091/runat_14062005_133459_9335/app_query.fasta_1.4238
-DB=UniProt_03 -QPMT=fastan -SUPFIX=n2p.rup -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bit6 -START=1 -END=-1 -MATRIX=bibosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6664091 @CCN 1 1 389 @runat_14062005 133459 9335 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_INDEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -WARN_INDEOUT=30 -THREADS=1 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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2250
2094.5
194.5
1691.5
1298.5
1282.5
1281
1271
1276.5
1271
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12) SEQUENCE FROM N.A. TISSUE-PCR rescued clones:	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	"Generation and initial analysis of more than 15,000 full-length human	Krzywinski M.I., Skaiska U., Smailus D.E., Schnerch A., Schein J.E.,	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		Hong L.,	., Moore T., Max S.I., Wang J.,	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	TISSUE=PCR rescued clones;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	Name=FLJ31547;	otein.	(TrEMBLrel. 27, Last	(TrEMBLrel. 27,	05-JJL-2004 (TrEMBLrel. 27, Created)	Q6NI32 FREHIMINARI; FRI; 3/3 FA.	

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Best Local Similarity:
Query Match:
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Pred. No.:
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; BC069501; AAH69501.1; -.
HSSP; P12337; 1K4Y.
GO: 0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00133; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00141; CARBOXYLESTERASE_B_2; 1.
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             GGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTAT
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25-OCT-2004 (TrEMBLrel. 28,

Last annotation update)

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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Ninomiya K., Takahashi-Pujii A., Hara H., Tanase T., Kusano J.,
RA Kanehori K., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yasia S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matanabe T., Sujimana Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Ayamazaki M., Watanabe T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikama Y., Okamoto S.,
RA Mizushima Sugano J., Satoh T., Shiral Y., Takahashi Y., Nakagawa K.,
RA Mizushima Sugano J., Satoh T., Shiral Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai Y., Yamashita R.,
RA Nakai K., Satoh T., Shiral Y., Takahashi Y., Nakagawa K.,
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XX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Altsusner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschulk C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altschulk C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altschulk C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altschulk C., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschulk C., Wagner B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschulk C., Woll C., Bonaldo M.F., Carninci P., Prange C.,

XX Altschulk C., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Altlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Altlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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XX Altlalon D.K., Muzny D.M., Sodergren E.J., Du X., Gibbs R.A.,

XX Altlalon D.K., Muzny M.M., Green E.D., Dickson M.C.,

XX Altlalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

XX Altlalon D.K., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altlalon D.K., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altlalon D.K., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                TISSUE=PCR rescued
Strausberg R.;
                                                                                                                                                                                                                                 "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Ota T., Suzuki Y., Nishikawa T., Ots
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIMILARITY: Belongs to the type-B
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InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE B 2;
Hydrolase; Hypothetical protein.
SEQUENCE 525 AA; 58200 MW; 7724878BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No . :
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                     246
                                            849
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GAGAAGAGTGAGGACCTGCAGGTGGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCT
                                 CACAAAGCCATCATGGAGAGTGGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTAT
                                                                  ValGlnLysAsnIleGluPheGheGlyGlyAspProSerSerValThrIlePheGlyGlu
                                                                                                                                 GTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAG
                                                                                                                                                                 TrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrp
                                                                                                                                                                              TGGGATCAGCATGCTCCGGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGG
                                                                                                                                                                                                              GluaspvalLeuvalvalvalGlnTyrArgLeuGlyIlepheGlyPhepheThrThr
                                                                                                                                                                                                                                                             GlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyr
                                                                                                                                                                                                                                                                                                                                                            HisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsn
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88.77%
88.25%
67.30%
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Matches:
Conservative:
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Q8NBC8
Q8NBC8;
01-OCT-2002
01-OCT-2002
01-OCT-2003
               Hypothetical protein FLJ33678
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
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                                                                                                                        PRELIMINARY;
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annotation updat
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               Euteleostomi;
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DB:
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                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamateu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa K., Pujimori K.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Cono Y., Takiguchi S., Watanabe M., Hara H., Tanase T., Kusano J.,
RA Kanehori K., Takabashi-Fujii A., Hara H., Tanase T., Kusano J.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Noriya S., Komai F., Hara R., Takeuchi K., Arita M., Sano S.,
RA Yoshikawa Y., Matanabe T., Sujawa A., Sasaki N., Actsuka S.,
RA Misagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Masagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Minomi Y., Xamada K., Fujii Y., Ozaki K., Hirao M., Kawakami B.,
RA Minomi R., Kawakami T., Noguchi S., Itoh T., Shiyata A., Fujiwara T.,
RA Ono T., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohnori Y.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Misai K., Yada T., Nakamira Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser estrs.
Pfam; PF00135; COseterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
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SEQUENCE
                                                                                                                                                                                                                                                                                 Match:
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GACGTGCTGGTTGTGGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGG
                                                                                                   ATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATC
                                            GlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyrGlu
                                                             GGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAG
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Matches:
Conservative:
Mismatches:
Indels:
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                                                    AATGAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTG
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Alignment Scores:
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RT "cauxin family protein.";

RT Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

C -! - SIMILARITY: Belongs to the type-B carboxylesterase/lipa

DR EMBL, AB186392; BAD35015.1; -.

DR GO: GO:0003824; F:catalytic activity; IEA.

NI InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002018; Ser_estrs.

NR InterPro; IPR000379; Ser_estrs.

NR PROSITE; PS00125; COesterase; 1.

R PROSITE; PS00125; CARBOXYLESTERASE B 1; 1.

R PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

M Hydrolase.

O SEQUENCE 575 AA; 63620 MW; 1005C35EB2E1183D CRC64:
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Q6AW47;
Q6AW47;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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                         AGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC
                                          GACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGA 1385
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SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Miyazaki M., Yamashita T., Taira H., Suzuki A.;

"cauxin family protein.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

EMBL, AB186393, BAD35016.1;

-GO; GO:0003824; F:catalytic activity; IEA.

InterPro; IPR000379; Ser estrs.

InterPro; IPR000379; Ser estrs.

Pfam; PF00112; CARBOXYLESTERASE_B_2; 1.

PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Carboxylesterase-like urinary excreted protein.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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C TISSUE-Temporal lobe right;
C TISSUE-Temporal N., Kusuda J., Tanuma R., Iseki K., Hirai M.
A Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.
Suzuki Y., Sugano S., Hashimoto K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
C -- SIMILARITY: Belongs to the type-B carboxylesterase/lip:
R EMBL; ABG60873; BAB4684.1; --
R HSSP; P12337; IK4Y.
R InterPro; IPR002018; CarbesteraseB.
R Pfam; PF00135; COesterase; 1.
W Hypothetical protein.
SEQUENCE 361 AA; 41032 MW; AC62AB6E78C5F1A1 CRC64;
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Q95KH3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI TaxID=9541;
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Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
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PIR; A47162; A47162.

HSSP; 077540; 1K4Y.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00379; Ser_estrs.

Pfam; PP00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
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"Molecular cloning and sequencing of thioesterase B cDNA and

"Molecular cloning and sequencing of thioesterase B gene associated with

stimulation of expression of the thioesterase B gene associated with

hormonal induction of peroxisome proliferation.";

J. Biol. Chem. 268:14278-14284(1993).

-I-FUNCTION. Fatty acid product is achieved by hydrolysis of the thio

ester by a thioesterase. This thioesterase may be associated with

peroxisome proliferation and may play a role in the production of

3-hydroxy fatty acid diester pheromones.

-I-TISSUE SPECIFICITY: Highest levels in uropygial gland, much lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE TISSUE=Uropygial gland; MEDLINE=93300823; PubMed=8314791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8839;
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GATCAACACATGCTC
                                 ValArgAspAlaAlaSerTyrProProMetCysLeuGlnAspLys------ValLeu
                                                                                                          LysProProValGlyProLeuArgPheSerGluProGlnProProGluProTrpLysGly 82
                                                                                                                                            GCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCCGCAGCCTGCATCGCCCTGGGATAAC
                                                                                                                                                                            ThrGlyGlnLysAlaGluGlnProGluValValThrAsnTyrGlySerValArgGlyTyr
                                                                     TTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTA
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Acyl-ester intermediate (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
N-linked (GloNAC. . .) (Potential).
; 03E35D90A037F6B0 CRC64;
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Conservative:
Mismatches:
Indels:
Gaps:
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 AAGGTGCATTACCCGAAATTCGGAGTGTCA
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177
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GTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGG 1520
                                                                                     GTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTT
                                                                                                                                 ProLeuPheValPheSerAlaValGluValAlaArgHisHisArgAspAlaGlyAsnPro
                                                                                                                                                      GTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCT
                                                                                                                                                                                                 CCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT---ATGAAGGAG 1175
                                                                                                                                                                                                                                                                     LeuAlaLeuSerPheLysGlyAlaProSerAspIleValAspLeuValTyrAsnGluTyr
                                                                                                                                                                                                                                                                                                                                    PheProGluPheThrGluGlyLeuGluLysAspValAlaArgGlnValLeuGlnSerThr
                                                                                                                                                                                                                                                                                                                                                                      GCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATC 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGCTTTCCTTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaGluMetGluGlnIleThrLeuLysMetProProMetPheIleSerAlaSerLeuAsp
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                                                                                                                                                                                                                                                                                                                 CTGCACATC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuPheThrGiu------GlnProGluGluGlnAlaGinArgIleAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTC
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RP SEQUENCE FROM N.A.

RC STRAIN=TVB/N; TISSUE=Colon, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rahas J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Holling M., Madan A., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

RA Jones S.J., Marra M.A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Q91WG0,

Q91WG0,

O1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-DC-2004 (TrEMBLrel. 28, Last annotation update)

25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
                                  STRAIN=FVB/N; TISSUE=Colon; Strausberg R.;
                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Ces2; Synonyms=ces2A3; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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   (JUN-2002) to the
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LysLeuLysGluArgLysMetGluPheTrpMetGlnLeuThrGluGlnIleMetSerAsp
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LysTyrTrpThrAsnDheAlaArgAsnGlyAsnProAsnGlyGluGlyLeuValH1sTrp 509
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ProGlnTyrAspMetAspGluArgTyrLeuGluIleAspLeuThrGlnLysAlaAlaLys 529
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Pred. No.:
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CSTRAIN=CS7BL/6; TISSUE=Liver;

X MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8;

RPUTIHATA T., Hosokawa M., Nakata F., Satoh T., Chiba K.;

Purification, molecular cloning, and functional expression of inducible mouse liver acylcarnitine hydrolase in C57BL/6 mouse, belonging to the carboxylesterase multigene family.";

Arch. Biochem. Biophys. 416:101-109(2003).

C-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family. EMBL; BC015290; AAH315290.1; -.

EMBL; BC034178; AAH34178.1; -.

EMBL; BC034178; AAH34178.1; -.

EMBL; BC034178; AAH34180.1; -.

EMBL; BC03419; AAH34191.1; -.

EMBL; BC03419; AAH34191.1; -.

EMBL; BC03419; AAH34191.1; -.

EMBL; BC03419; BAC76623.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005615; C:extracellular space; TAS
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
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SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE=Colon,
Strausberg R.;
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TTCCCAGGAGGTGCCTTCAAGACTGGCTCCAGCCTCCATCTTTGATGGGTCCGCCCTGGCT
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                                                                                                                          AspMetLysMetMetLeuSerSerPhePro-----MetSerGluAspCysLeuTyr
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Name=9030624102...
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; C:
               STRAIN=C57BL/GJ; TISSUE=Cvary and uterus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002)
      "RIKEN integrated sequence
                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAINE-57BL/6J; TISSUE-Ovary and uterus;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, clone:5031415B19 product:similar
to CARBOXYLESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Ovary The FANTOM Consortium,
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Sciurognathi; Muridae;
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; DOI=10.1038/35055500;
(RISA) system-384-format
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Alignment :
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Best Local Similari
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RA KITANSE=2238B257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Histeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gyunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Gubbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Ra Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodrighez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Townski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakzume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       PROSITE; PS00122; (PROSITE; PS00941; (Pydrolase. SEQUENCE 559 AA;
                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: Belongs to the EMEL AKOT7248; BACG6707.1; -. EMBL; BC055062; AAH55062.1; -- HSSP; P12337; IKAY.
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MGD; MGI:2443170; 9030624L02Rik.
GO; GO:0006515; C:extracellular space;
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
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STRAIN=C57BL/6J; TISSUE=Ovary
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TE; PS00122; CARBOXYLESTERASE_B_1;
TE; PS00941; CARBOXYLESTERASE_B_2;
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TISSUE=Colon;
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, Akimura T., A
, Hanagaki T.,
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GlyGlnAspSerAlaSerProlleArgAsnThrHisThrGlyGlnValArgGlySerLeu

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                                                                               GlnGluLeuMetAlaSerLysAspPheHisProValProSerIleIleGlyIleAsnAsn
                                                                                                                                                                ACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTG
                   ATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTC
                                                                                                                                      AsnSerGluThrLeuMetCysCysLeuArgGlyLysAsnGluAlaGluMetLeuAlaIle
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GO; GO:0016787; F:hydrolase activity; II
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000886; ER_target_S.
InterPro; IPR000379; Ser_estrs.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE B 2;
PROSITE; PS000041; ER_TARGET; UNKNOWN 1.
Hydrolase: Signal
PROSITE; PS(
PROSITE; PS(
Hydrolase; (
SIGNAL
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SEQUENCE
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O35533;
O1-JAN-1998 (TrEMBLrel. O5, Created)
O1-JAN-1998 (TrEMBLrel. O5, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                    Pergamon,
                                                                                                                                              STRAIN-Syrian golden; TISSUE-Liver; Sone T., Ishida Y., Takabatake E., Wang C., Is submitted (MAY-1995) to the EMBL/GenBank/DDBJ-1-SIMILARITY: Belongs to the type-B carboxyl EMBL; D50577; BAA23605.1; -.
                                                                                                                                                                                                                                                 "Microsomal amidases and carboxylesterases.";
(In) Guengerich F.P. (eds.);
COMMRRHEMSIVE TOXICOLOGY VOLUME 3, Biotransformation,
Pergamon, Oxford (1997).
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STRAIN-Syrian
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carboxylesterase.
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carboxylesterase/lipase
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STRAIN-C57BL/60; TISSUE=Colon;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA (Meth. Enzymol. 303:19-44(1999).
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MIS musculus adult male colon cDMA, RIKEN full-length enriched
1ibrary, clone:9030624L02 product:similar to CARBOXYLESTERASE (EC
3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE).
                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                               cloning
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DOI=10.1038/35055500;
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Best Local Similarity:
Query Match:
DB:
                               US-10-023-515-1 (1-2158) x Q8BM97 (1-559)
                                                                                                                      Percent Similarity:
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X MEDLINE-20530313; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE-20530313; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE-20530313; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE-20530313; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE-20530313; PubMed=110.1101/gr.152600;

X MEDLINE-20530313; PubMed=110.1101/gr.152600;

X Monda K., Itch M., Aizawa M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., X Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., X Yamamoto R., Matsumoto H., Izawa M., Oleyama E., Watshiki M., X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., X Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

YA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format gequencing pipeline with 384 multicapillary sequencer.";

10 Genome Res. 10:1757-1771(2000).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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Nature 420:563-573(2002).
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GO; GO:0005615; C:extracellular space;
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
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                                                   LysSerThrAlaLeuLysMet 379
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RA MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Q6PDB7;
05-JUL-2004 (T:
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05-JUL-2004 (T:
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Hypothetical pri
Name=BC015286;
         SEQUENCE FROM N.A
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                  Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                        mouse cDNA sequences.";
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(TIEMBLrel. 27, Last sequence update)
(TIEMBL. 27, Last annotation updat
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                                            99:16899-16903(2002)
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Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00279; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Hydrolase; Hypothetical protein.
SEQUENCE 556 AA; 61927 MW; 58DE05A33C7
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the type-B carboxylesterase/lipase
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EMBL; BC058815; AAH58815.1;
HSSP; P12337; 1K4Y.
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AACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTC
                                                                                                                                                                                                     GTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGG
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Matches:
Conservative:
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- LeuGlyValMetLysGluIleLysLeuLysLeu
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AC Q6GM5
DT 05-JU
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                                                                                                                                    AGCACCATCCCC-----CTGATCCTGTCTGCCTCCGACATGCTCCACACTCCTCTT
                                                                                                                                                                   LeuAspThrGlnProAlaValGlyArgAlaLeuLysSerArgArgLeuGlnPheTrpThr
                                                                                                                                                                                                                                                                                                  GluLysLeuLeuSerArgArgMetMetLysTyrTrpAlaAsnPheAlaArgHisGlyAsn
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                                                                                                 LysThrLeuSerGlnLysIleGlnGluLeuArgAlaSerGlnAspLysHisThrGluLeu
                                                                                                                                                                                                  CTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACC
                                                                                                                                                                                                                                                                    GlyTyrPhePheTrpAspMetLysLeuAspPhe-----
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GlyIleTyrGlyThrGluAspAlaArgProLeuLeuThrThrAsnTyrGlyGlnLeuLeu

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                                                                                  Query Match:
DB:
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Best Local Similarity:
                                          US-10-023-515-1 (1-2158) x Q6GM54 (1-568)
                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                      Alignment
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Koewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.S., Schutz J., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.S., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.S., Schutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.S., Schutz J., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski A.S., Schutz J., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski A.S., Schutz J., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski A.S., Schutz J., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski A.S., Schutz J., Schutz J., Schutz J., Schutz J., Schutz J., Schutz J., Schutz J., Schutz J., Schutz J., Schutz J., Sc
                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
LOC443703 protein (Fragment).
Name=LOC443703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                    Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Gerhard D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               initiative.",
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  225:384-391 (2002) .
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CARBOXYLESTERASE_B_2;
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64.49%
48.22%
32.63%
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297

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AlaLeuPro---PheValHisSerPheThrSerValValProPheIleMetGluGiuTyr
                                                                                                                                                                     GAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCAC
      ATCCCGCCTCAGTATTTGCAC----
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PRELIMINARY; PRT; 561 AA.
O70177;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
                                                                                                                                                                                                            SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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serGluAspPheHisProValProSerIleIleGlyValAsnThrAspGluTyrCysCys
              CAGAAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGGCTTC 1157
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ValValGlyMetAlaSerMetTyrAspGlySerLeuLeuThrValAsnGluAspLeuVal 173
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                                                                                                                                              GACCTGCAG---GTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTG
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-DB=ISSUEd_Patents_AA -QFMT=fastan -SUFFIX=n2p_.rai -MINMATCH=0.1 -LOOPCL=0
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US-10-023-515-1	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarit Query Match: DB:	13 942.5 2 16 942.5 2 17 940.5 2 17 940.5 2 18 940.5 2 19 80.5 2 20 80.5 2 20 80.5 2 21 789.5 2 22 78.5 2 23 777.5 2 24 777.5 2 24 777.5 2 25 775.5 2 26 774.5 1 30 764.5 1 31 764.5 1 33 764.5 1 33 764.5 1 33 764.5 1 34 769.5 1 35 764.5 1 36 764.5 1 37 764.5 1 37 764.5 1 38 764.5 1 39 761.5 1 39 761.5 1 39 761.5 1 39 761.5 1 39 761.5 1 39 761.5 1 39 761.5 1 39 761.5 1 39 761.5 1 31 759.5 1 41 759.5 1 42 759.5 1 43 759.5 1 44 759.5 1 45 755.5 1 46 759.5 1 47 759.5 1 48 759.5 1 49 THE REFERENCE CURTAIT CURTAIT FILING PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR PRIOR APPLICATI PRIOR PRIOR APPLICATI PRIOR PRIOR APPLICATI PRIOR PRIOR APPLICATI PRIOR PRIOR APPLICATI PRIOR PR
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                                       GATGGTGCTTTCCTTACTGAGCCTCTAGATCTATTGTCTCAGAAAAGCATTTAAAGCA 1115
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                                          APPLICANT: Danks, Mary K.

APPLICANT: Potter, Philip M.

APPLICANT: Houghton, Peter J.

ITILE OF INVENTION: Compositions and Methor
ITITLE OF INVENTION: Compositions and Methor
ITITLE OF INVENTION: Tumor Cells

FILE REFERENCE: SO-005

CURRENT APPLICATION NUMBER: US/09/595,682B

CURRENT FILING DATE: 2000-01-16

PRIOR APPLICATION NUMBER: 60/075,258

PRIOR FILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: PATENT OF SEQ ID NOS: 30

ORGANISM: Homo sapiens

US-09-594-6878-78
 Alignment Scores:
Pred. No.:
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Percent Similarity:
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                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRANCESQ for Windows Version 4.0

SEQ ID NO 6426
Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                    ORGANISM: Human
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| IlevalGlyValAsnAsnAsnGluPheGlyTrpLeuIleProLysValMetArgIleTyr 357
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APPLICANT: VENUER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,488

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
US-10-023-515-1 (1-2158) x US-09-949-016-9670 (1-577)
                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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AspThrGlnLysGluMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr
                              GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCTCCATCTGATACAAAAC 1232
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US-09-595-682B-21
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APPLICANT: Houghton, Peter J.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
FULE REFERENCE: SJ-0005
FULE REFERENCE: SJ-0005
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FULE REFERENCE: PATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATEITIN Ver. 2.0
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GTCAATAACCACGAGTGTGGCTTCCTGCCTATG------
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         US-10-023-515-1 (1-2158)
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Rabbit
US-09-264-737-2
                                                                                                     Score:
                                                                                                                Alignment Scores: Pred. No.:
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US-09-264-737-2
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                                                                                                                                                                                                            TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(1051) RLE3 Pyridine Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LANCOUNT SCC
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APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
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                                                                                                                                                                                                      LENGTH: 566
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GlylleTrpGlyPhePheSerThrGlyAspGluHisSerArgGlyAsnTrpGlyHisLeu 193
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LysAlaProAlaGluIleLeuAlaGluLysLysTyrAsnMetLeuProTyrMetValGly 349
                                 GlyAspProLysGluAsnThrAlaPheLeuThrThrValIleAspGlyValLeuLeuPro
                                                                                                                                                                     CCCTCCAAGGAGCTGCTG-----ACCCTCAGCCAGAAA-----
                                                                                                                                                                                                   IleGluAlaGlyCysLysThrThrThrSerAlaValMetValHisCysLeuArgGlnLys
                                                                                                                                                                                                                                    CATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAA 998
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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
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APPLICANT: Houghton, Peter J.
APPLICANT: Houghton, Peter J.
FILE OF INVENTION: Compositions and Methods
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1998-02-19
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PRIOR FILING DATE: 1999-02-12
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SOFTWARE: Patentin Ver. 2.0
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                                                                                                                              TYPE: PRT ORGANISM: Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08845295A
Patent No. 5817490
; GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Proc.
TITLE OF INVENTION: Ascorbic Acid,
TITLE OF INVENTION: 2-Keto-L-Gulon.
NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
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US-08-845-295A-2
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diek

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/84:

FILING DATE: 25-April-97
                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: P.
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| LysAlaProAlaGluIleLeuAlaGluLysLysTyrAsnMetLeuProTyrMetValGly 348
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                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                          Eastman Chemical Company
  UMBER: US/08/845,295A
25-April-97
                                                                                                                                                                                                                                                                                                                                                                       Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, and 2-Keto-L-Gulonic Acid
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Percent Similarity:
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; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-845-295A-2
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APPLICATION NUMBER: US 60/017,87;
PILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REGISTRATION NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFPAX: 423-229-1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
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Matches:
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Indels:
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TyrAspGlnGluGlyTyrLeuGlnIleGlyValAsnThrGlnAlaAlaLysArgLeu 556
                                                                                 ACCTITGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCA-----GCT 1646
                                                                                                                                                                                        CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
                                                                                                                                                                                                             GlnTyrArgProSerPheSerSerAspLysPheThrLysProLysThrValIleGlyAsp
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                                             TATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTC 1706
                                                                     AsnPheAlaArgSerGlyAsnProAsnGlyGluGlyLeuProHisTrpProPheThrMet 536
                                                                                                                                                                HisGlyAspGluIlePheSerValPheGlyPheProLeuLeuLysGlyAsp------
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                                                                                                                 -AlaproGluGluGluValSerLeuSerLyBThrValMetLyBPheTrpAla
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RESULT 9
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                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                       US-09-140-933-2
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Patent No. 6022719
GENERAL INFORMATION:
APPLICANT: Hubbs, Jo
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

PILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,9:
FILING DATE: 27-August-98
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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ZIP: 37662-5075
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CITY: Kingsport
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                      GlnProAlaSerProProValValAspThrAlaGlnGlyArgValLeuGlyLysTyrval
                                                                     SerLeuGluGlyLeuAlaPheThrGlnProValAlaValPheLeuGlyValProPheAla
                                                                                                                                            , Application US/09140933
                                                                                                                                                                     TrpLeuLeuProLeuValLeuThrSerLeuAlaSerSerAlaThrTrp-----AlaGly
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Matches:
Conservative:
Mismatches:
Indels:
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                                               TATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCAC-----
                                                                                              GGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAG 1253
                                                                                                                      MetGlyPheProLeuSerGluGlyLysLeuAspGlnLysThrAlaThrSerLeuLeuTrp 394
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LysSer-----ProGlu
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RESULT 10
US-09-146-661-2
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                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,
FILING DATE: 03-Septmeber-98
CLLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: BRZYM
TITLE OF INVENTION: ASCOT
                                        TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

PILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432

TELEPHONE: 423-229-6.89
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
COMPUTER: GYONEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE:
              TYPE: Amino Acid
TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Kingsport
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                          GlnIleAlaValLeuAlaGlyCysLysThrThrThrSerAlaValPheThrPheValHis
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RESULT 11
US-09-150-515-2
J Sequence 2, Application US/09150515
Patent No. 6271006
GENERAL INFORMATION: Enzymatic Process for the Manufacture TITLE OF INVENTION: ASCORDIC Acid, 2-Keto-L-Gulonic Acid, TITLE OF INVENTION: 2-Keto-L-Gulonic Acid, 2-Keto-L-Gulonic Acid, 2-Keto-L-Gulonic Acid, 3-Keto-L-Gulonic Acid, 3-Keto-L-
                                    STREET: P.O. Bo
CITY: Kingsport
                                                        ADDRESSEE: Eastman Chemical Company STREET: P.O. Box 511
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TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-150-515-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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Best Local Similarity:
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TELEPHONE: 423-229-6189
TELEPHX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IS COMPUTER: OF AIRCH GIBK
COMPUTER: IBM COMPATABLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,:
FILING DATE: 09-SEP-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/017,:
APPLICATION NUMBER: US 60/017,:
APPLICATION NUMBER: 38,346
REGISTRATION NUMBER: 38,346
REGISTRATION NUMBER: 38,346
REGISTRATION NUMBER: 70432
TRIECOMMINICATION THORMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . No.:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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TCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGAC----GTGCTGGTTGTGGTC
                                                                                                                                             TTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACA 515
                                              ArgGlyArgLeubrovalMetValTrpIleHisGlyGlyGlyLeuValLeuGlyGlyAla
                                                                                            GGCTCCAAGCTCCCGTCTTGGTGTGGTTCCCCAGGAGGTGCCTTCAAGACTGGCTCAGCC
                                                                                                                                                                                                                                                                                                                                                                        CTCTTAGAT-----
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Amino Acid
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-96; 25-April-97
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                                      HisGlyAspGluIlePheSerValPheGlyPheProLeuLeuLysGlyAsp------
                                                                                        GlnTyrArgProSerPheSerSerAspLysPheThrLysProLysThrValIleGlyAsp
                                                                                                                                        ProValLysLysLysAspLeuPheLeuAspLeuMetGlyAspValValPheGlyValPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAA-----GCATTTAAA 1112
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                                                                                                                  CGGCACCGGCCTCAGTGCTTTGAAGAC-----ACGAAGCCGGCTTTTGTCAAAGCCGAC
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TYPE: PRT
ORGANISM: Rabbit
     115
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|LeuProValMetValTrpIleHisGlyGlyGlyLeuMetValGlyGlyAlaSerThrTyr 134
                                 CTCCCCGTCTTGGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTT 584
                                                                 SerGluAspCysLeuTyrLeuAsnIleTyrThrProAlaAspLeuThrLysArgGlyArg 114
                                                                                                 TCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAG 524
                                                                                                                               HisMetLeuSerGluLeuPheThrAsnArgLysGluAsnIleProLeuLysPhe-----
                                                                                                                                                                                              AsnThrThrSerTyrProProMetCysSerSerAspAla------ValSerGly 76
                                                                                                                                                                                                                                GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAA 428
                                                                                                                                                                                                                                                                                                                                                                                           ProSerAlaPro---ProValValAspThrValLysGlyLysValLeuGlyLysPheVal
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1034.50
55.05%
42.24%
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Matches:
Conservative:
Mismatches:
Indels:
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 	CTGAAGGGGGACATTGTTATGTTGGAAGGAGGGGGGGGGG	1452 CCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGTGCTTC 1511	GlyAlaBroThrTyrMetTyrGluTyrArgTyrArgProSerPheSerSerAspMetArg		1332 CTTGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCT 1391 ::: :::			1170AAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTT 1211 343 GluGlvLvsLeuAerclTlvsThrallandrollt.			10/4 AAIGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC		1032ACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTTC	::: ::: ThrGluGluGluLeuMetGluV	ThrSerAlaValMetValHisCysLeuArgGlnLys	CATTICTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGAGGTGCCTGAGGACAAAA	227 SerSerLeuPheArgLysAsnThrLysSerLeuAlaGluLysIleAla 242	207 SerProLeuThrLysAsnLeuDheHHsargAlaileSerGluSerGlyValAlaLeuLeu 226 885 CCTTACCTGGAGGCCCATCATTATTATCACACACACACAC	825 TCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATC 884	187 GlySerValThrIlePheGlyGluSerAlaGlyGlyGlnSerValSerIleLeuLeuLeu 206		GACCAGGTGGCTCTGTCCTGGGTCCAGAGAGAGAGAGAGTGCCTGTGTGTG	645 GGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAG 704	
QY 468 GAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC 527	US-10-023-515-1 (1-2158) x US-08-446-100-26 (1-454)	24.34% Indels: 3 Gaps:	Percent Similarity: 942.50 Matches: 200 Percent Similarity: 59.33\$ Conservative: 64 Best Local Similarity: 44.94\$ Mismatches: 150	No.: 3.44e-83 Length:	US-08-446-100-26	YES YES	; TOPOLOGY: unknown ; MOLECULE TYPE: protein ; HYPOTHETTOAL. vec	; TELEFAX: (703) 425-2767 ; INFORMATION FOR SEQ ID NO: 26: ; SEQUENCE CHARACTERISTICS:	KET NUME ON INFOF 703) 425	; NAME: Hendricks, Glenna ; REGISTRATION NUMBER: 32,535	FICATION: 439 AGENT INFORMA	CURRENT APPLICATION DATA:	5	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: TAM DC COMPANIA	; STATE: VA ; COUNTRY: US ; ZIP: 22031	STREET: 9669 A Main Street, P.O. Box 2509 CITY: Fairfax	NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ADDRESSE: Moderate of the control of the contr		GENERAL INFORMATION: APPLICANT: Broomfield, Clarence A	US-084-46-100-26 Sequence 26, Application US/08446100 Patent No. 6001626	508	Qy 1692 CTCGGACAGAGACTCAAAGAACCGCGGGGGTTTTTTTTTT	Qy 1632 TCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTTACCTCCAGCTGGACTTGAACATGAGC 1691 Db 488 ProGlnTrDProAldTyvAsgTvrLvaGluGlvTvrLaglatic Classes Co.	Db 468 MetValMetLysTyrTrpAlaAsnPheAlaArgAsnGlyAsnProAsnGlyGluGlyLeu 487

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CTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC 527
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                                                                      GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGA 1541
                                                                                                                                                                                                                              CTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGG 142
                                                                                                                                                                                                                                                                                                                         VallysLysLysAspLeuIleLeuAspLeuIleAlaAspValMetPheGlyValProSer
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                                            GluLeuPheSerValPheGlyAlaProPheLeuLys------GluGly
                                                                                                                                      TyrArgProSerPheSerSerAspMetLysProLysThrValIleGlyAspHisGlyAsp
                                                                                                                                                                                  CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGAT 148
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                               US-10-023-515-1 (1-2158) x US-08-446-100-28 (1-454)
                                                              Query Match:
DB:
                                                                                               Best Local Similarity:
                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                            US-08-446-100-28
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                                                                                                             Percent Similarity:
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INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/446
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                             .
No.:
                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: br
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
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TELEPHONE: (////
(703) /
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STATE: VA
COUNTRY: US
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 468 GAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC 527
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Matches:
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                                                                                Indels:
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1482 GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGGACATTGTTATGTTCGAAGGA 1541
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                                                                                  CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGAT 1481
                                                TyrArgProSerPheSerSerAspMetLysProLysThrVallleGlyAspHisGlyAsp
                                                                                                                        ValileValalaargasnHisargaspalaGlyalaproThrTyrMetTyrGlupheGln
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                                                                                                                                                                                                                  ACTGAAATCCGAGACAGTCTTCTGGACTTGGTTGGAGATGTGTTCTTTGTGGTCCCTGCA 1361
                                                                                                                                                                                                                                                               {\tt IleAlaLysGluLeuIleProGluAlaThrGluLysTyrLeuGlyGlyThrAspAspThr}
                                                                                                                                                                                                                                                                                                  ATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTG 130
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                                                                                                                                                                                                                                                                                                                                    GlyGlnLeuAspGlnLysThrAlaMetSerLeuLeuGlySerProIleProLeuPheAla 277
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               Query Match:
DB:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   FRAGMENT TYPE: NORIGINAL SOURCE: ORGANISM: huma
                                                                                                                                                                                                                    MOLECULE IL
                                                                                                                                                                                                                                        TOPOLOGIE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                     No.
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STREET: 500
CITY: Fairfax
TMATE: VA
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ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA
COUNTRY: U:
ZIP: 22031
                                                                                                                                                                                                                                                                          STRANDEDNESS: sing TOPOLOGY: unknown
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US-10-023-515-1 (1-2158) x US-08-446-100-30 (1-454)
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                                        CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGAT 1481
                                                                             GluThrGlnArgHisSerThrLeuLeuGlyThrVallleAspGlyMetLeuLeuLeuLys 217
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|ProValMetValTrpIleHisGlyGlyGlyLeuMetValGlyAlaAlaSerThrTyrAsp
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                                                                                                                    CTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGG 1421
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                                                            1662 CAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTG 1721
                                                                                                                                                                1542 GCCACGGAGGAGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 1601
432 AlaPheTrpThrAsn 436
                                              GlyTyrLeuGlnIleGlyAlaAsnThrGlnAlaAlaGlnLysLeuLysAspLysGluVal 431
                                                                                            GATTTTTGGACCAGC 1736
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Search completed: June 15, 2005, 08:57:14 Job time: 63.6132 secs

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Post-processing: Minimum Match 0%
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-Q=Cgm2 1/USPTO spool/6664091/runat 14062005 133501 9433/app query.fasta 1.4238
-DB=Published Applications AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pot -THR MXX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=6664091 @CGN 1 1 295 @runat 14062005 133501 9433
-NCFU=6 -ICFU=3 -NO MMAP -LARGEQUERY -NGESCORES=0 -WAITGABOD=10 -XGAPEXT=0.5
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_n2p.model -DEV=xlh
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 US-10-023-515-2

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Sequence 2, Application US/10023515

Sequence 2, Application US20020182636A1

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023,515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 581
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Sequence 2, Application US/10674636
Publication No. US20040086922A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT FILING DATE: 2003-09-29
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; PRIOR APPLICATION NUMBER: 60/256,369;
; PRIOR FILLING DATE: 2000-12-18;
; PRIOR APPLICATION NUMBER: 60/279,508;
; PRIOR FILLING DATE: 2001-03-28;
; NUMBER OF SEQ ID NOS: 6;
; SOFTWARE: FASTSEQ for Windows Version 4.0;
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| Sequence 46, Application US/10757262 | Publication No. US/20040197825A1 | GENERAL IMPORATION: MINISTREET | GENERAL IMPORATION: METHODS AND COMPOSITIONS FOR TREATING APPLICANT: Silos-Santiago, Inmaculada | APPLICANT: Silos-Santiago, Inmaculada | APPLICANT: Silos-Santiago, Inmaculada | APPLICANT: Silos-Santiago, Inmaculada | APPLICANT: Silos-Santiago, Inmaculada | TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING | 10405, 18560, 2047, 1171LE OF INVENTION: 1405, 636, 4421, 5410, 3005, 2045, 14405, 18560, 2047, 1171LE OF INVENTION: 3975, 5387, 2167, 2277, 2245, 2487, 2397, 82112, 14990, 1171LE OF INVENTION: 3270, 4899, 14303, 16816, 17827, 32620, 577, 619, 1423, 1171LE OF INVENTION: 2543, 9625, 1587, 2277, 2245, 2287, 52908, 69112, 14990, 1171LE OF INVENTION: 2543, 9625, 1587, 15885, 16623, 730, 2395, 2554, 8675, 1171LE OF INVENTION: 2543, 9625, 1587, 15885, 16623, 730, 757, 619, 1423, 1711LE OF INVENTION: 2543, 9625, 15402, 16209, 16386, 21165, 30911, 41897, 1643, 1711LE OF INVENTION: 2543, 9625, 13231, 32409, 84260, 2882, 8203, 32678 OR FILLE OF INVENTION: 2543, 9625, 13231, 32409, 84260, 2882, 8203, 32678 OR FILLE OF INVENTION NUMBER: US 60/440,318 PRIOR APPLICATION NUMBER: US 60/440,318 PRIOR APPLICATION NUMBER: US 60/440,318 PRIOR APPLICATION NUMBER: US 60/440,78 PRIOR APPLICATION NUMBER: US 60/440,78 PRIOR APPLICATION NUMBER: US 60/440,78 PRIOR APPLICATION NUMBER: US 60/440,78 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/440,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPLICATION NUMBER: US 60/470,76 PRIOR APPL
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Best Local Similarity:
Query Match:
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LENGTH: 581
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FILING DATE: 2003-09-26
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HAPPLICANY: GLEAN ONCE COMPOUNDS

FILE REFERENCE: GP50039

FILE REFERENCE: GP50039

CURRENT APPLICATION NUMBER: US/10/451,168

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR PILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-03

PRIOR PILING DATE: 2001-02-06,797

PRIOR PILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR PILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR PILING DATE: 2001-03-19

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PRIOR PILING DATE: 2002-06-28

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NUMBER OF SEQ ID NOS: 110

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1 SEQ ID NO 91

1 EXECUTE: 575
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RESULT 5
US-10-433-256-10
Sequence 10, Application US/10433256
Publication No. US20040081980A1
GENERAL INFORMATION:
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G. APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R. APPLICANT: AU-YOUNG, Janice K.; BRUGHN, Mariah R. APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HAFALLA, Apyril J.A.; TANG, Y. Tom
APPLICANT: UU, Dyung Aina M.; LAL, Pereti G.
APPLICANT: WARREN, Bridget A.; YANG, Junming
APPLICANT: GANDHI, Narinder K.; NGUYEN, Danniel B.
APPLICANT: GANDHI, Narinder K.; NGUYEN, Danniel B.
APPLICANT: ISON, Craig H.
APPLICANT: ISON, Craig H.
APPLICANT: OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0313 USN
CURRENT APPLICATION NUMBER: US/10/433,256
PRIOR APPLICATION NUMBER: US/10/433,256
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2000-12-08
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PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2001-01-01-02-02
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL PROGRAM
SEQ ID NO 10
LENGTH: 642
TYPE: PRT
ORGANISM: Homo mapiens
PEATURE:
PRIOR FILING BATE: 2001-02-02
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; OTHER INFORMATION: Incyte ID No: 6538080CD1
US-10-433-256-10
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RESULT 6
US-10-451-168-92
; Sequence 92, Application US/10451168
; Publication No. US20040091989A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: FOT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,99
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
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PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NOS: 110
ORGANISM: Homo sapiens
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                                    ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg
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Matches:
Conservative:
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Indels:
Gaps:
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GAGGAGGAGTTACTGAGCCGGAAGATGATGAATATACTGGGCTACCTTTGCTCGAACC 1607
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APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZIKO
APPLICANT: ISHII, SHIZIKO
APPLICANT: HIO, YURI
APPLICANT: HIO, YURI
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APPLICANT: HIO, YURI
APPLICANT: HIE, RYOTARO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGHON, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILER REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-01-28
PRIOR APPLICATION NUMBER: 50/350,435
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 381
PRIOR APPLICATION PRIOR SERVICES PRIOR FILING DATE: 2001-09-14
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US-10-094-749-2375
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ISOGAI, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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1388 424	1329 TIGCTIGGAGAIGIGTTCTITGIGGICCCIGCACIGATCACAGGCTCGATAICACAGAGAI	
1328 405	1269 GCTAATGAATACTTCCATGACAAGCACTCCCTGAACTGAAATCCGAGACAGTCTTCTGGAC	
1268 385	1209 CTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTG	
1208 365	1149 TGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCC	
1148 345	1089 CTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGAGTCAATAACCACGAG 	
1088 325	1029 AAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	
1028 _. 305	969 GAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAG	
968 285		
908 265		
848 245	789 TCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTC	
788 225	729 GTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAG 	
728 205	98	
668 185	09 GAGGACGTGCTGGTTGTGGTCCTCCAGTACCC	
608 165	549 GGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTAT	
548 145	489 ATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCA	
488 125	429 CACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAAC 	
428 105	9 GAAGCCACCTCCTACCCTAAT	

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APPLICANT: Padigaru, Muzalidhara
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Sangolli, Esha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Casman, Stacie J.
APPLICANT: Liete, Mario W.
APPLICANT: Liete, Mario W.
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rochenberg, Mark E.
APPLICANT: Rochenberg, Mark E.
APPLICANT: Rochenberg, Mark E.
APPLICANT: Rochenberg, Mark E.
CURRENT APPLICATION NUMBER: U$20040030110A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: 00/2011-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,36
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,863
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
Padigaru, Muralidhara
Shimkets, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Casman, Stacie J.
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Miller, Charles E.
Malyankar, Uriel M.
Spytek, Kimberly A.
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Li, Li
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Patturajan, Meera
Liu, Ziaohong
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PRIOR APPLICATION NUMBER: 60/281,906
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR PILLING DATE: 2001-04-06
PRIOR PILLING DATE: 2001-04-06
PRIOR PILLING DATE: 2001-04-06
PRIOR FILLING DATE: 2001-04-10
PRIOR FILLING DATE: 2001-04-10
PRIOR FILLING DATE: 2001-04-10
PRIOR PFILING DATE: 2001-04-12
PRIOR FILLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILLING DATE: 2001-04-13
PRIOR FILLING DATE: 2001-04-17
Remaining Prior Application data removed - 10
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 196
LENGTH: 581
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     GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA
                        TrpValGlnLysAsnileGluPhePheGlyGlyAspProSerSerValThrilePheGly
                                  TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC
                                                              CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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Sequence 2, Application US/10381898
Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; BAUGHN,
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                                                                    TACCTCCAGCTGGACCTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTTGGAT
                                                                                                                                           TyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluProArgArgAsp
                                                                                       TTTTGGACCAGCACCATCCCC 1745
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APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: RAWLZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: RAWLZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REPERENCE: PI-0233 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/247,581
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                                                                                                                                                                                                                                                                                                                                                      LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incy
 172
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                                                       AspAlaGlyAlaProValTyrPheTyrGluPheArgHisArgProGlnCysPheGluAsp
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Sequence 2219, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

ITILE OF INVENTION: No. US20030236392A1e1 full length cDM.

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: US/10/104,047

PRIOR APPLICATION NUMBER: 2002-03-25

PRIOR APPLICATION NUMBER: SOFTMARE: PAGE ID NOS: 4096

SOFTMARE: PAGENTIN Ver. 2.1

SEQ ID NO 2219
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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; ORGANISM: Homo sapiens
US-10-104-047-2219
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Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 2, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masso
TITLE OF INVENTION: CAT KIDNEY DISE
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; FILE REFERENCE: SHIG FFUZUSUO
CURRENT APPLICATION NUMBER: US/10/233,933A
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
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ORGANISM: Felis catus
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                                                                                           GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProIleAlaAsnGlyLeu
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                                        PheHisLysAlaIleMetGluSerGlyValAlaIleLeuProLeuLeuMetArgProPro
                                                         TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTG----GAGGCCCAT
                                                                                                            GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA
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Conservative:
Mismatches:
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                                     APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
ITILE DE INVENTION: CAT KIDNEY DISEASE MARKER
FILE REPERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOPTWARE: PATENTIN VEY: 2.0
SEQ ID NO 4
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               LENGTH: 54
TYPE: PRT
 ORGANISM: Felis catus
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US-10-023-515-1 (1-2158) x US-10-233-933A-4 (1-542)
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CURRENT FILING DATE: US/10/451/168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US/10/45232
PRIOR FILING DATE: 2000-12-17
PRIOR PELING DATE: 2000-12-17
PRIOR PELING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
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PRIOR FILING DATE: 2001-04-04
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Publication No. US20040091969A1
GENERAL INFORMATION:
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APPLICANT: SMITHKLINE BEECHAM p.l.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
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US-10-451-168-93
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SOFTWARE: PASTSEQ for Windows Version
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                                 CGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCT
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GRGANISM: Homo sapie
FBATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: X
US-09-925-298-689
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
UNMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 689
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Best Local Similarity:
Query Match:
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Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
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                                              411 TGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAA 470
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                       PheLeu-----SerGlnPheAsnMetThrPheProSerAspSerMetSerGlu
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                                                    HisGlyAspGluLeuProPheValPhe---ArgSerPhePheGlyGlyAsnTyrIleLys 465
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APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA103plC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEG ID NOS: 846

SOFTWARE: PatentIn Ver. 2.0

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TYPE: PRT
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Publication No. US20030054421A1
GENERAL INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: SITE
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   411 TGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAA 470
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| (gn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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ALIGNMENTS

721 CTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGATGGGGTG 780 721 CTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGATGGGGTG 780 781 GCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGGAGTGGGGTG 780 781 GCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGTGGAGTGGGTT 840 781 GCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTT 840 781 GCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGTGCCTGAAGGACA 900 841 GCACATTTCTGTGGTAACAATGCGTCAGACTTATGAGAAGAAGAGTGAGT	
RESULT 2 US-10-674-636-3 Sequence 3, Application US/10674636 Publication No. US20040086922A1 GENERAL INFORMATION: APPLICANT: CURTIS, RODY A. J. APPLICANT: S108-Santiago, Inmaculada ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF FILLE REFERENCE: 10448-122001 CURRENT APPLICATION NUMBER: US/10/674,636 CURRENT FILING DATE: 2003-09-29 PRIOR APPLICATION NUMBER: US/10/023,515 PRIOR FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: 60/256,369 PRIOR APPLICATION NUMBER: 60/256,369 PRIOR APPLICATION NUMBER: 60/279,508 PRIOR FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 1746 TYPE: DNA ORGANISM: Homo sapiens US-10-674-636-3 Query Match 100.0%; Score 1746; DB 18; Length 1746;	OY 1141 CTGCACATCCCGCCTCAGTATTTGCACCTTTGTGCCTTAATGAATACTTCCATGAACAACCAC 1200 1141 CTGCACATCCCGCCTCAGTATTTGCACTTATTGAATTACTTCCATGAACAACCAC 1200 1201 TCCCTGACTGAATACCGAACACGTCTTCTGCTTGCATGAACAACCAC 1200 1201 TCCCTGACTGAATCCGAACACGTCTTCTTGCTTGCTTGCATGAACAACCAC 1200 1201 TCCCTGACTGAATCCGAACACGTCTTCTTGCTTGCTTGCT

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                                      Sequence 1, Application US/10023515
; Sequence 1, Application US/10023515
; Publication No. US20020182636A1
; GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT APPLICATION NUMBER: 60/256,369
pRIOR APPLICATION NUMBER: 60/256,369
pRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 2158
TYPE: DNA
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Sequence 1, Application US/10674636
Publication No. US20040086922A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR APPLICATION NUMBER: 05/256,369
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
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; PRIOR APPLICATION NUMBER: 60/27;
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ FOR WINDOWS VG
; SEQ ID NO 1
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1838)
US-10-674-636-1
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RESULT 5
US-10-757-262-45
VS-10-757-262-45
Sequence 45, Application US/10757262
Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu
APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bliasof, Scott D.
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TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: UROLOGICAL DISORDERS US; TITLE OF INVENTION: 1405, 636, 4421, 5410, 7111  
FOR INVENTION: 33751, 52872, 14063, 2017  
TITLE OF INVENTION: 33751, 52872, 14063, 2017  
TITLE OF INVENTION: 33751, 52872, 14063, 2017  
TITLE OF INVENTION: 32720, 4809, 14303, 1586, 1171  
TITLE OF INVENTION: 2543, 9626, 13231, 3240;  
TITLE OF INVENTION: 2543, 9626, 13231, 3240;  
TITLE OF INVENTION: 25953  
FILE REFERENCE: MPIO3-007PIRNOMNIM CURRENT APPLICATION NUMBER: US (0/440,318  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: US (0/444,783  
PRIOR APPLICATION NUMBER: US (0/444,783  
PRIOR APPLICATION NUMBER: US (0/457,901  
PRIOR APPLICATION NUMBER: US (0/457,901  
PRIOR FILING DATE: 2003-02-04  
PRIOR FILING DATE: 2003-05-08  
PRIOR APPLICATION NUMBER: US (0/468,775  
PRIOR APPLICATION NUMBER: US (0/471,614  
PRIOR APPLICATION NUMBER: US (0/478,742  
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TYPE: DNA
ORGANISM: Homo sapiens
FRATURE;
NAME/KEY: CDS
LOCATION: (96)...(1841)
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OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
OF INVENTION: 53010, 16852, 1587, 2207, 22245, 4,3239, 4373, 51164,
OF INVENTION: 18547, 115, 579, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
OF INVENTION: 32720, 4809, 14303, 1586, 17827, 32620, 577, 619, 1423,
OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
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Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1654; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Matches 1654; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	1728 A Homo sapiens	PRIO PRIO PRIO PRIO PRIO NUMB	PRIOR FILING DATE: 2000-12-20 PRIOR APPLICATION NUMBER: 60/260,482 PRIOR FILING DATE: 2001-01-09 PRIOR APPLICATION NUMBER: 60/264,922 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: 60/266,797 PRIOR FILING DATE: 2001-02-06	מכסרטרטם	-10-4 Seque Publi GENER APPL APPL APPL	Oy 1741 CCTTGA 1746 Db 1836 CCTTGA 1841	1681 AGTCCTCTTTCCTTAACTTTCCTCTCTCTCCTCCAGCCTTTCTTT	Db 1656 ACTGAGCAGTACCTCCAGCTGAACCATGAGCCTCGAACAAGAACCG 1715 Qy 1621 CGGGTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGCTCTGCCTCCGACATGCTCCAC 1680	Db 1536 GAAGGAGCACGGAGGAGAAGATACTTACTGAGCCGGAAGATGATGAATAATACTGGGCTACC 1595 Oy 1501 TTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTG 1560
TCCCTTGCCCTCCATCTGATACAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT TCCCTTGCCCTCCATCTGATACAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT GTGGCTAATGAATACTTCCCATGACAAGCACTCCCTGACTGA	1051 GAGTGTGGCTTCCTGCTGCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAG	Qy 931 CAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCCTTAATGAGCCTCTA 990	Qy 811 TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC 870	Qy 691 GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA 750	Qy 571 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGTTCC 630	Db 433 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 492 Oy 511 TATGAGGACGTGCTGGTTGTGGTCGTCAGTACCGGCTAGGAATATTTGGTTTCTTCACC 570	373 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGGGTTCC 451 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCC	Qy 331 CAACACATGCTCAAGGTGCATTACCCGANATTCGGAGGTGCAGAAGACTGCCTCTACCTG 390	Qy 211 CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270

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APPLICANT: ANNANALA, Madhusudan M.; YAO, Monique G. APPLICANT: ANJANAMALA, Madhusudan M.; YAO, Monique G. APPLICANT: ARVIZU, Chandra S.; RING, Huijun Z. APPLICANT: LEE, Extractine A.; DING, Li
APPLICANT: LEE, Extractine A.; DING, Li
APPLICANT: VUE, Henry; TRIBOULEY, Catherine M.
APPLICANT: VUE, Henry; TRIBOULEY, Catherine M.
APPLICANT: UL, Dyung Aina M.; LAL, Preeti G.
APPLICANT: UL, Dyung Aina M.; LAL, Preeti G.
APPLICANT: WARREN, Bridget A.; YANG, Junming
APPLICANT: GANDHI, Ameena R.; LU, Yan
APPLICANT: LSON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0313 USN
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/267,706
PRIOR FILING DATE: 2001-02-02
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                                                                      NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL Program
SEQ ID NO 23
LENGTH: 2232
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATTON: Incyte ID
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Best Local Similarity 99.5
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    CAATAACCACGAGTGTGGCTTCCTGCTGC
             CAATAACCACGAGTGTGGCTTCCTGCTGCTGATGAAGGAGGCTCCTGAGATCCTCAGTGG
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g g	Quer Best Matc	US-10-	PRI PRI SOF	CUR CUR	; Publ ; GENE ; APP	RESULT US-10-	<u>ት</u>	<u> </u>	ß &	<u>ል</u>	B 8	B 8	ት δ	B 8	B 8	ያ ያ	<u> </u>
91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCCAGGCTGGGATGGAT	Query Match 93.4%; Score 1631.2; DB 17; Length 2092; Best Local Similarity 99.2%; Pred. No. 0; Matches 1653; Conservative 0; Mismatches 3; Indels 10; Gaps 1;	LENGTH: 2092 TYPE: DNA ORGANISM: Homo sapiens 10-104-047-249	PRIOR FILING NORTH. PRIOR FILING DATE: NUMBER OF SEQ ID NOS: 4096 SOFTWARE: Patentin Ver. 2.1 SEG ID NO 249	•	Publication No. US20030236392A1 GENERAL INFORMATION: APPLICANT: HELIX RESEARCH INSTITUTE APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20030236392A1el full length cDNA	RESULT 8 US-10-104-047-249 ; Sequence 249, Application US/10104047	1701 TTTCCTCTCTCCTCCAGCCTTTCTTTTTCTTTTTGTGCTCCTTGA 1746	1641 CACCATCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCTT	1581 GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTTGGACCAG 1640	1521 TAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGA	1461 GAAGTTACTGAGCCGGAAGATGATGATAATACTGGGCTACCTTTGCTCGAACCGGGAATCC 1520	1401 GTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGA 1460 	1341 CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT 1400 	1281 ATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTG 1340	1221 CAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGGTCG 1280	1161 TTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA	1101 CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTA 1160
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RESULT 9

US-10-114-270-195

Sequence 195, Application US/10114270

Publication No. US20040030110A1

GENERAL INFORMATION:

APPLICANT: Guo, Xiaojia

APPLICANT: Kekuda, Ramesh

APPLICANT: Miller, Charles E.

APPLICANT: Malyankar, Uriel M.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Sytek, Kimberly A.

APPLICANT: Liu, Ziaohong

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Li, Li

APPLICANT: Li, Li

APPLICANT: Exthusen, Bryan D.

APPLICANT: Sernas, Linda

APPLICANT: Gorman, Linda

APPLICANT: Gorman, Linda

APPLICANT: Gorman, Carol E.A.

APPLICANT: Smenoy, Suresh G.

APPLICANT: Smenoy, Suresh G.

APPLICANT: Smenoy, Glennda

APPLICANT: Smenoy, Glennda

APPLICANT: Smithson, Glennda
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APPLICANT
           NT: Ji, Weizhen

NT: Anderson, David W.

NT: Liete, Mario W.

NT: Rastelli, Luca

NT: Rastelli, Luca

NT: Edinger, Shlomit R.

NT: Stone, David J.

ANT: MacDougall, John R.

ANT: MacDougall, John R.

ANT: Rothenberg, Mark E.

DF INVENTION: NO. US20040030110A1el Pr
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
Padigaru, Muralidhara
Shinkets, Richard A.
Gangolli, Esha A.
Taupler Jr., Raymond J.
Camman, Stacie J.
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; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 195
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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PRIOR PILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR PILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,710
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PRIOR APPLICATION NUMBER: 60/283,710
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PRIOR APPLICATION NUMBER: 60/283,710
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PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
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Best Local Similarity 95.3%;
Matches 1496; Conservative
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CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
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PRIOR APPLICATION NUMBER: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/US01/49232

PRIOR FILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR FILING DATE: 2000-12-09

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR PILING DATE: 2001-^^
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PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 41
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 95.4%;
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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
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OR FILING DATE: 2001-01-09
OR APPLICATION NUMBER: 60/264,922
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: 60/266,797
OR FILING DATE: 2001-02-06
OR APPLICATION NUMBER: 60/276,988
OR APPLICATION NUMBER: 60/276,988
OR APPLICATION NUMBER: 60/281,535
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SOFTWARE PERL Program
SEQ ID NO 20
LENGTH: 1857
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7473645CB1
US-10-381-898-20
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APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: CANDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: RAWIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: RAWIZU, Chandra S.; POLICKY, Jennifer L.;
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APPLICANT: RAWIZU, Chandra S.; POLICKY, Jennifer L.;
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APPLICANT: RAWIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: RAWIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
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Best Local Similarity 94.7%;
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                                                                                                                                                                                                                                                                                                                                                                             ; Score 1386.2; ; Pred. No. 0; 0; Mismatches
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CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACGACGACGATGAAGTCCGCTTTGT
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APPLICANT: HO, YURI
APPLICANT: NAGAI, KEIICHI
APPLICANT: NAGAI, KEIICHI
APPLICANT: RIB, RYOTARO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 736
LENGTH: 1962
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-094-749-736
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US-10-094-749-736
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Publication No. US20030219741A1
GENERAL INFORMATION:
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Best Local Similarity
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                            CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTTGG 1635
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APPLICANT: MANSAITAN

APPLICANT: MANSAITAN

TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006

CURRENT APPLICATION NUMBER: US/10/233,933A

CURRENT FILING DATE: 2002-09-03

PRIOR APPLICATION NUMBER: JP2002-057908

PRIOR FILING DATE: 2002-04-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 2145

TYPE: DNA
ORGANISM: Felis catus
PEATURE:
NAME/KEY: CDS
LOCATION: (175)...(1803)

FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
COLATION: (1804)...(2145)

OTHER INFORMATION: n is a, c, g, or t

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Matches 1329; Conserv
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                                                                                                                                      CTGGACTTGCTTGGAGATGTGTTTTTGTGGTCCCTGCACTGATCACAGCTCGATATCAC
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                                                          AGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAA 1347
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Sequence 1, Application US/1023393A

Publication No. US20040214171A1

GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Myazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006

CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION UNMBER: US/10/233,933A
CURRENT FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1629
TYPE: DNA
CORGANISM: Felis Catus
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                   CTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
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                                                                             GETGCCTTCCTGAAAGGCGACATTGTCATGTTCGAAGGAGCCACCGAGGAGGAGAAATTG
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FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-09
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 110
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US-10-451-168-42
i Sequence 42, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION;
APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; APPLICANT: GLAXO GROUP LIMITED
; APPLICANT: GLAXO GROUP LIMITED
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; ORGANISM: Homo
US-10-451-168-42
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Matches 1022; Conservative
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                                CCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGAT
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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11160.423 Million cell updates/sec
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ALIGNMENTS

RESULT 1

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Qy 241	181	Qy 181	Db 121	Оу 121	Db 61	Ογ 6	Db	Q	Query Match Best Local Sin Matches 1746;	ORIGIN	FEATURES BOUTCE	H	TITLE		ORGANISM		S	VERSION	Z		AR438765
CCGCAGCCTGCATCGCCCTGCGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGC	AACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCCGCTGGGATCCCTGCGATTTACGAAC	AACGTGTTCCTCGGAGTCCCCCTTTGCTGCTCCCCCGCTGGGATCCCCTGCGATTTACGAAC	ACCAGGCTGGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTG	ACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTG	CTGTTGGGACACAGACAGTGGGGAAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAAC	61 CTGTTGGGACACAGACAGTGGGGGAAAAACTGGGGCCTTCTGCTGAAGGGCCACAGAGAGGAAC 1	1 ATGCCACAGGGACTTACTTCATCTGCTTCACAATGGTGCTTTTTTCCTGATTCTCCAGCCC 60	1 ATGCCACAGGGACTTACTTCATCTGCTTCACAATGGTGCTTTTTTCCTGATTCTCCAGCCC 60	Query Match 100.0%; Score 1746; DB 6; Length 1746; Best Local Similarity 100.0%; Pred. No. 0; Matches 1746; Conservative 0; Mismatches 0; Indels 0; Gaps		location/Qualities 11746 /organism="unknown" /mol type="genomic DNA"	: US 6664091-A 3 16-DEC-2003;	Curtis, R.A.J. and Silos-Santlago, I. 53010, a human carboxylesterase family member and uses thereof	1 (bases 1 to 1746)	Unknown. Unclassified.	Unknown.		AR438765.1 GI:42663740	Sequence 3 from patent US 6664091.	AR438765 1746 bp DNA linear PAT 20-FEB-2004	
300	240	240	180	180	120	120	J	Ü	0;											04	

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CCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAG
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Millennium Pharmaceuticals, Inc. (US)
Cocation/Qualifiers
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53010, a novel human carboxylesterase family member
thereof
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
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Curtis, R.A.J. and Silos-Santiago, I.
53010, a human carboxylesterase fam
Patent: US 6664091-A 1 16-DEC-2003;
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Millennium Pharmaceuticals, Inc. (U
Location/Qualifiers
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53010, a novel human carboxylesterase family member
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	REFERENCE AUTHORS	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 5 BC069501 LOCUS DEFINITION	₽ :	\$ ₽ t	8 음 1	\$ B \$	S B &	?	P 5	}	}) B 5	? B \$	5 B 1	Ş B
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,	3 1 (bases 1 to 2047) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C., Altachul, S.F., Zeebbarg, B., Buetow, K.H., Schaefer, C.	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidas	MGC:97182 IMAGE:7262427), complete cds. BC069501 BC069501.1 GI:46854682 MGC.		 1836 CCTTGA 1841	1776 AGTCCTCTTCCTTAACTTTCCTCTCTCTCCCAGCCTTCTTTTTCTTTTGTGCT 1835	1716 CGGGTGGATTTTTGGACCAGCACCATCCCCTGATCCTGTCTGCTGCTGCACATGCTTTTTTTT	1621 CGGGTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGCCTCCGACATGCTCCAC									1116 ATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAG

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COMMENT
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          Query Match
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Director MGC Project.
Direct Submission
Submitted (29-ApR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, &
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
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Proc. Natl. Acad. Sci. U.S.A.
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Patent: WO 0246426-A 313-JUN-2002;
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/mol_type="unassigned DNA"
/mb.xref="taxon:9606"
/mote="Incyte ID No: 6538080CB1"
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De 151 CTCCCCCTTORANGCCCTCTACCTACTACACCCCCACCTCCCCACCCCCCCCC	Query Match 93.4%; Score 1631.2; DB 6; Length 2092; Best Local Similarity 99.2%; Pred. No. 0; Matches 1653; Conservative 0; Mismatches 3; Indels 10; Gaps 1; Qy 91 GGGCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGCATCAGGGCAAGCAA	JOURNAL Patent: EP 1308459-A 249 07-MAY-2003; Helix Research Institute (JP); Research Association for Biotechnology (JP) FEATURES Location/Qualifiers Source 12092 12092 12093 /organism="Homo sapiens" /mol_type="mRNA" /mol_type="mRNA" /db_xref="taxon:9606"					1461 GAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCC	Db 1524 CITTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTTGT 1583 Oy 1401 GTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGA 1460		Db 1344 TTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA
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Ota, T., Suzuki, Y., Mishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Xawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Sato, K., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Sato, K., Kikkawa, K., Pujimori, K., Tanai, H., Kimata, M., Watanabe, M., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Miraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takayuchi, S., Watanabe, S., Yosikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzuni, Y., Fujimori, Y., Komiyama, M., Tashima, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Jikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Inagaki, H., Jikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RS Isogai, T. and Yamamoto, J.

RS Isogai, T. and Yamamoto, J.

RS Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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                                                                                                                                                                                                                              Similarity
                                                                  Genet. 36 (1), 40-45 (2004)
                                                                                                                                                                                   Conservative
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/db_xref="GI:21749269"
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/clone_lib="BRAWH2"
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/db_xref="taxon:9606"
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passed the following selection analysis.		281 ATATCACAGAGATGCTGGTGCACCTGTCTATGAGTTTTCTGGCACTGATCACAGCTCG 133	8
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Kowis, C.R., Sneed, A.J., Mar A.N., Gibbs, R.A.		1161 TTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA	B 8
<pre>center code: BCM-HGSC Web site: http://www.hgsc.bcm Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M.</pre>		88	P \$
cDNA Library Preparation: Lif cDNA Library Arrayed by: The DNA Sequencing by: Baylor Col Sequencing Center		98 1	§ § §
NIH-MGC Project URL: http://m Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Tech	COMMENT	981	, 음 성
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Mammalia; Butheria; Primates 1 (bases 1 to 2298) Strausberg, R. Direct Submission	REFERENCE AUTHORS TITLE	861 TGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCT 920 	B &
	KEYWORDS SOURCE ORGANISM	801 GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA 860 	B 8
Homo sapiens, similar to mRNA. BC039073 BC039073.1 GI:25058132	ACCESSION VERSION	741 CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA 800	B 8
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38 81		501 CCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGG 560	g 8
521 578		98	B 3
1461 GAAGTTACTGAGCCGGAAGATGATGI 	Db Qy	381 CCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGGTCTT 440	р У
1401 GTTCGGTGGTGCCTTCCTGAAGGGG	da Vo	321 GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTG 380 	당 상
1341 CTTTGAAGACACGAAGCCGGCTTTTV 	Qy Db		B &
	_	258 CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 317	Ъ

/organism="Homo sapiens"

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lone distribution information can be found msortium/LLNL at: http://image.llnl.gov w: k Column: 18 or full length sequencing because it ction criteria: Hexamer frequency ORF
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ancer Genomics Office, National Cancer
ve, Room 11A03, Bethesda, MD 20892-2590,
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Life Technologies, Inc.
The I.M.A.G.E. Consortium (LLNL)
College of Medicine Human Genome
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                                                                                                           A.M., Lu, X., Hulyk, S.W., Loulseged, H., Martin, R.G., Muzny, D.M., Nanavati,
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ites; Catarrhini; Hominidae; Homo.
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/clone="IMAGE:5174937"
/tissue_type="Brain, Lung, T
/clone_Tib="NIH_MGC_115"
/lab_host="DH10B"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                         Homo sapiens
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                                                    GI:42314969
                                 (human)
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         Chordata;
Primates;
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nt WO02068579.
         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Patent: WO 02068579-A 18978 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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              ĠŦĊĀĠĀĊŦĊŦĠĀĠĠĊĊĊŦĠĊŦĠĀĠĠŦĠĊĊŦĠĀĠĠĀĊĀĀĀĀĊĊĊŦĊĊĀĀĠĠĀĠĊŦĠĊŦĠĀĊ
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/mol_type="unassigned DNA"
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Mammalia; Eutheria; !
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                 GTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGA 1516
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nilarity 94.7%;
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/mol_type="unassigned DN/

/db_xref="taxon:9606"
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Primates;
                                                                    Score 1386.2;
Pred. No. 0;
0; Mismatches
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Catarrhini; Hominidae;
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861 TGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCT 920		
Scheetz, T. S., Brownstein, J., Usdin, T. B., TOSHIYUKI, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Scheutz, J., Wyers, R.M., Enterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) REFERENCE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) REFERENCE Strausberg, R. Direct Submission Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, URANAK NIH-MGC Project URL: http://mgc.nci.nih.gov Comment: MgC help desk Email: cgapbs-remail.nih.gov Tissue Proccurement: Baylor Human Genome Sequencing Center	ON NO DAN H &	Db 1335 CAGTCTTCTGGACTTGGTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCG 1394 Oy 1281 ATATCACAGAGATGCTGGTGCACCTGTCTATGAGTTTCGGCACCGGCCTCAGTG 1340

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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbe, R.A.
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CCAGGAGGTGCCTTCAAGACTGGCTCCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 5	391 AACATCTATIGOGCCCACGCCGATACAGGCTCCAAGCTCCCCGGTCTTGGTGTGTGGTTC 450	331 CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG 390	271 CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 330	342 CCCCGCTGGGATTCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 401	GTCACTGTGCGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT	222 GGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATTGGATTCAGGGCAAGCAA	91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	Y Match 17.0%; Score 1344.4; DB 6; Length 1962; Local Similarity 90.9%; Pred. No. 0; hes 1505; Conservative 0; Mismatches 1; Indels 150; Gaps 1;		Helix Research Institute (JP), Biotechnology (JP) Location/Qualifiers		1 Isogai,T., Sugiyama,T., Otsuki Yamamoto,J.I., Isono,Y., Hio,Y	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia. Entheria. Drimares. Catarrhini. Hominidas. Homo	0N Sequence 736 from Patent EP1293569. N AX714052 AX714052.1 GI:29888980		CTCCTCCAGCCTTTCTTTTTCTTTTGTGCTCCTTGA	CICCICAGCCITICITITICITITGIGCTCCITGA 1746	1651 CTGATCCTGTCTGCCCTCCGACATGCTCCACACAGTCCTCTTTCTT	1591 ATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCC 1650	
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1531 GACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAAC 1590	14/1 AGCCGGAAGATGAAGATACTIGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC 1530		1422 1421	1422 1421 1351 ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGT 1410	1362 GACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGA 1421 1291 GATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGAC 1350	31 GACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGA	1171 GTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA	1111 TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT 1170	1051 GAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAG 1110 	991 GATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCAGGAGTCAATAACCAC 1050 	1062 CAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	02 TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGC	42	811 TATGAGAAAGGGTGGAGGTGGCACATTTCTGTGGTAACAATGCGTCAGAC 870		762 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTTGGC 821 691 GAGTCCGCGGGGAGCCATAAGTTTTTTTTTTTTTTTTTT	TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC	5/1 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC 530	42 TATGAGGACGTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC	582 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 641 511 TATGAGGACGTGCTGGTTGTGGTCGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC 570

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                                                                                Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamorto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                NEDO human cDNA sequencing project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC

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461

401 270

CAGAAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 330 CCCCCCCTGGGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG CCCCCGCTGGGATCCCCTGCGATTTACGAACCCGCAGCCTGCGATCGCCCTGGGATAACTTG GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT 341 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT 210

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Matches 1505;
                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics Laboratory; 1532-3 Yana, Kisarzau, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Bconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Submitted (24-OCT-2001) Takao Isogai, Kisarazu, Chiba 292-0812, Jap
      Conservative
                                                                                                                        /note="cloning vector: pME18SFL3~mRNA from NT2 neuronal precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction.~majorly NT2 neuron"
                                                                                                               SLTFLSLLQPFFFFCAP"
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=_lib="NT2RI2"
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                      Score 1344.4;
Pred. No. 0;
  Mismatches
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Published Only in Database (2004)
2 (bases 1 to 1728)
Miyazaki,M., Yamashita,T., Taira,H. and SuDirect Submission
Submitted (04-AUG-2004) Masao Miyazaki, RIResearch, Supra-Biomolecular System Resear Wako-shi, Saitama 351-0198, Japan
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Canis familiaris cauxin mRNA for carboxylesterase-like urinary
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Research Group; Hirosawa 2
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Search completed: June 14, 2005, 22:52:51 Job time: 7589.61 secs

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1 (bases 1 to 742)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLMN1451 row: k column: 09 High quality sequence stop: 740.
                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can
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                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5181056"
/lab_host="DH10B"
                              /clone lib="NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
                      021. Note: this is a NIH_MGC Library."
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genuther based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Plate: LLAM11435 row: 1 column: 10
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
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                                                                             quality sequence start: 6 quality sequence stop: 565.
/organism="Homo sapiens"
/mol_type="mRNA"
                                       1. .576
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                                                         1 (bases 1 to 1680)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                       AY414459.1 GI:39770421
                                                                                                                                                                                                                                                                                       genomic survey sequence
                                                                                                                                                                                                                                                                                                           Homo sapiens CES2 gene,
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                                       Inferring nonneutral evolution from human-chimp-mouse orthologous
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larity 96.4%;
Conservative
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//clone lib="NIH MGC 115"
//note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
   302 (5652), 1960-1963 (2003)
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/clone="IMAGE:5174937"
/lab_host="DH108"
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Pred. No. 3.8e-107;
0; Mismatches 14;
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VIRTUAL
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GSS 17-DEC-2003

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partial sequence,

Kejariwal, A.,

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Submitted (16-NOV-2003) Celera
Rockville, MD 20850, USA
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, N.D. and Cargill, M.
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GTGGCGTGGCCCTGCCCGGCCTCATTGCCAGCTCAGCTGA----TGTCATCTCCA
                     GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC
                                                       TGTCTTCGCTTGTTGTCCCCCATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGA
                                                                           TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCCATCATCGAGA
                                                                                                                              TCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTG
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/locus_tag="HCM5231"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.1e-104;
0; Mismatches 639;
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

REFERENCE

RESULT 5 AK033563 LOCUS

DEFINITION

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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GS RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yok Kanagawa 230-0045, Japan (B-mail:genome-reseggc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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Please visit our web site for further details.
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TTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGT
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                                                                                                                                                                                                                                                                                    GTCGTCCAGTACCGGCTAGGAATATTTTGGTTTCTTCACCACATGGGATCAGCATGCTCCG
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                                                                                                                                                              GGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAG
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/db_xref="GI:26329245"
/db_xref="GI:26329245"
/db_xref="GI:26329245"
/translation="MPLYKLGWILNAVACGVLLLVLHVQGQDSASPIRNTHTGQVRGS
LVHVKOTDIAVHTELGIPFALPPUGPLRFAPPEAPEASGVEDGTSHPNMCLQNDNLM
GSEDLKMMNLILPPISMSEDCLYLNIYVPAHAHEGSNLPVMVWIHGGALTVGWASMYD
GSMLAATEDVVVVAIQYRLGGVLGFFSTGDQHAKGNMGYLDQVALKWVQQNIYHFGGN
PDRVTIFGESAGGTSVSSHVVSPMSQGLFHGALMSWGYLDDLISSSSEMVHRIVAN
LSGCAAVNSTTLMCCLRGKNEAEMLAINKVFKIIFGVVDGEFLJKHPQELMASKDFHP
VPSIIGINNDEYGWILPTIMDPAQKIEEITRKTLPAVLKSTALKMMLPPECGDLLMBE
TMGDTEDPETILQAGFEEMKGGDFMFVIFALQVAHFQRHAPVFFEFGHFPSFKDFRD
TMGDTEDPETILAGAFFEEMKGGDFMFVIFALQVAHFQRHAPVFFEFGHFPSFKDFRD
TMGDTEDPETILAGAFFEEMKGGDFMFVIFALQVAHFQRHAPVFFEFGHFPSFKDFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVMDHDEQYLQLDIQPSVGRALKARRLQFWTKTLPQKIQELKGSQERHKEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83% ID, 100% length, match=1677)
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/clone lib="RIKEN full-length enriched
/dev stage="adult"
25. .1704
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Pred. No. 4.2e-102;
0; Mismatches 647;
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SOURCE

AK077248 LOCUS AK077248 DEFINITION Mus musculus 11 days pregnant adult female ovary and RIKEN full-length enriched library, clone:5031415B19 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.
5 01
1600 GGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCCCTGA
543
1540 CTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAG
1483 ATGATGAAGTACCGGGCCAACTTTGCACGGCACGGGAACCCCCAACAGTGAGGGTCTACCC
1480 ATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATC
. 4
1420 AAGGGGACATTGTTATGTTATGGAAGGTTTCCTTGTCTTTGGCTACCAGTTCGGT
1 6
1300 GCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCG
1258 GGGACTTCATGTTCGTGATCCCTGCACTACAAGTAGCACATTTTCA-
1240 GGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGT
1180 GAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTT
1138 CTAAAAAGCACAGCCCTAAAAAATGATGCTGCCTCCTGAGTGTGGTGACCTGCTAATGG
1120 CTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAAT
1072 ATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGC
1012 TITAAAGCAATTCCTTCCATCATCAGAGTCAATAACCACGAGTGTGGCTTCCTGCTGC
958 GGTGTGGATGGAGAGTTCCTACCCAAGCATCCTCAGGAGCTGATGGCCTCTAAGGA
952 CGAGTGGTTGATGGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCA
898 CTAAGAGGCAAGAATGAAGCAGAGATGCTGGCTATTAATAAGGTCTTCAAAATCATCCCC
892 CTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGC
w
3
772 AGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTG
724 GTGTCTTCACATGTTGTGCCCCCATGTCCCAGGGACTCTTCCATGGTGCCATCATGAG
712 GTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA
664 CACTTTGGAGGCAACCCTGACCGAGTCACCATTTTTGGAGAGTCAGCGGGTGGCACAAGT

COMMENT

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cDNA library was prepared and sequenced in Mouse Genome cDNA library was prepared Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                              Direct Submission
Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham RIKEN Yokohama C30-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                             Adachi, J., Aliawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Horti, F., Imotani, K., Ishii, Y., Ich, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahasahi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RIKEN Genome Exploration.
FANTOM Consortium.
Functional annotation of a full-length
Functional 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (Dases I to 2687)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium and the RIKEN Genome Exploration Research
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mammalia; Eutheria;
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Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers
                                                                                        GCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACT
                                                                                                                                                                          TACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCAC
                                                                                                                                                                                                                                          TIGIGCCTCCAGAACTCAGAGIGGCTGCTCTTA---GATCAACACATGCTCAAGGIGCAT
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GGCATGGCTTCCATGTATGATGGATCCATGCTGGCAGCAACTGAGGATGTGGTGGTGGTC
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                                                                     CTGCCTCCCATCTCTATGTCTGAGGACTGCCTGTATCTCAACATCTATGTACCAGCCCAT
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/db xref="GI:26346112"
/db xref="GI:26346112"
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pyvkadhgdbiflvfgygpgniklptpftplalgystakpvgmapfarhenpry
pyvkadhgdbiflvfgygpgniklptpftygygpgniklptpftgbfpym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product; putative similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (METHYLBUTYRASE) [MESOCTICETUS BUTTALES] (SPTR | 03533, evidence: FASTY, 03$10, 100$length, match=1677)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVMDHDEQYLQLDIQPSVGRALKARRLQFWTKTLPQKIQELKGSQERHKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Bex="female"
/tissue type="ovary and uterus"
/clone lib="RIKEN full-length enriched mouse
/dev_stage="11 days pregnant adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="putative"
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                           is Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hirmoto, K., Hiraoka, T., Hircozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myzaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Ohazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Ohazaki, Y., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagama, M., Tagawa, A., Takahashi, F., Takawa, A., Takahashi, Takaku, A., And Hayashizaki, Y., Takawa, A., Takahashi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                    Nature 420, 563-573
6 (bases 1 to 4927)
                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AKO40349

MUS MUSCULUS 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430088E12 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE) (MEGOCTICETUS auratus), full insert sequence.
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Location/Qualifiers
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Please visit our web site for further details.
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ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
[Mesocricetus auratus] (SPTR (O35533, evidence: FASTY,
70.7%ID, 99.2%length, match=1672)"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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/strain="C57BL/6J"
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E 6 (Dases 1 to 1958)

Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hiramoto,K., Hiraoka,T., Hirozane,T., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kasukawa,T., Kojima,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Myazaki,R., Ohno,M., Ohsato,N., Nakamura,M., Nishi,K., Nomura,K., Myazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sasohe,Y., Tagami,M., Tagawa,A., Shinagawa,A., Shiraki,T., Sagabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramateu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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1958 bp mRNA linear HTC 03-APR-2004

Mus musculus adult male cecum cDNA, RIKEN full-length enriched
library, clone:9130231C15 product:similar to LIVER CARBOXYLESTERASE
PRECUESOR (EC 3.1.1.1) [Mesocricetus auratus], full insert
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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URL:http://fantom.gsc.riken.jp/.
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Please visit our web site for further details.
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                                                                                                                                                                                            TTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTAC
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prvtipgvsaggtsvsshilspmskglehgaingsgyallpdlisdtsevykkyvanl
gccatdsealhclarkskdeilaingvpkmipavdgeflpkhpgelltsmdphpv
bsicotdecggvpmpmgldbiiknitretlpavvdgeflpkhpgesthlveey
mgdtedetloappremklgdpymfvipalgvahfgrgapvyfyvefghlsseinkyrps
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/clone="9130231C15"
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Tmotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                    Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANTOM Consortium.
Functional annotation of a full-length Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute c
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute c
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC
RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yok
KAINEN YOKOHAMA (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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                                                                                                        CCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGGACCTGTCTACTTCTATGA 1319
                                                                                                                                                                                      CGCTGAAGGCAAACTGGACCAGAAGACAGCCAATTCTCTCTTGTGGAAGTCCTACCCAAC 1220
                                                                                                                                                                                                                                                                                                                                                                                                     AGTGGGCATCAACAAGCAAGAGTTTGGCTGGATCATTCCAACGCTTATGGGCTATCCACT 1160
                                      GTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCA 1379
                                                                                                                                                                                                                                              ACTTAAAATCTCTGAGAATATGATTCCAGTGGTCGCTGAGAAGTATTTAGGAGGGACAGA
                                                                                                                                                                                                                                                                                CCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCA 1199
                                                                                                                                                                                                                                                                                                                                                                TCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC---AT 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCCTGTGTGAAGGAGG-----C 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGCCAAAGGCACCAGAAGAGATCCTGGCTGAGAAGAGTTTCAGCACTGTCCCCTACAT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĊTTĀĊTTGGĀĀĀTCCĀĀĀĀGĀGĀĠĊTATCCCŤTCCŤĊCĊŤACTĠŤĠĀŤŤĠĀŤĠĠĀĠTĀGŤ
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1460

translation="MTAQSRSPTTPTFPGPSQRTPLTPCPVQTPRLGKALIHCWTDPG

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FEATURES
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SOURCE
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/dermany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZ)(34N9935) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomeforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZ9434N0935 further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2888)

Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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AL713761
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                                                                                                                                 /gene="DKFZp434N0935"
954. .2777
                                                                                                                                                                                                                /tissue type="testis"
/clone_Tib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites Not1 + Sall"
/dev_stage="adult"
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/db_xref="UniProt/Swiss-Prot:000748"
                                                                                      /gene="DKFZp434N0935"
/codon_start=1
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/db_xref="rZPD:DKFZP434N0935"
/db_xref="taxon:9606"
                                                                                                                                                                                           note="carboxylesterase 2"
                                                                                                                                                                                                                                                                                                        clone="DKFZp434N0935"
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QPLGEQQRVRRQRTETSBPTMRLHRLRARLSAVACGLLLLLVRGQGQDSASPIRTTHT
GQVLGSLVHVKGANAGYQTFLGIPFAKEPLGPLRFAKPEGSRLVRGGVTHFPAMCL
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LKNIREPHMKADHVKTTEEESQLSRKMMSYWANFARNGNPNGCLFHWPLFDQEEQYL QLNLQPAVGRALKAHRLQFWKKALPQKIQELBEPEBRHTEL"

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ORIGIN Best Local Similarity Matches 850; Conserv Query Match 1906 1846 1786 1666 1606 1546 1486 1426 1366 1306 1246 2020 1726 1960 893 833 773 713 653 593 533 473 413 353 296 236 176 116 CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGTTCCCCAGGAGGTGCCTTCAAGACTG ACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACG AGGTGGTTGCACATTTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCC TCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTG GGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGT TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGG GCATGGCTTCCTTGTATGATGGTTCCATGCTGGCTGCCTTGGAGAACGTGGTGGTCA GCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCCTATGAGGACGTGCTTGTGG GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGATCCACGGTGGTGCGCTTGTTTTTG TCCCTTCCGACTCCATGTCTGAGGACTGCCTGTACCTCAGCATCTACACGCCCGGCCCATA 1545 TGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA---TCAACACATGCTCAAGGTGCATT CACCCCTGAGCCCCTGAATCTTGGAGTGGTGTGAGGGATGGAACCACCCATCCGGCCA 1425 GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG GGAACACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGC 175 TGCGGGGCAAGAGTAAAGAGGAGATTCTTGCAATTAACAAGCCTTTCAAGATGATCCCCG CGGTGGTGGCCAACCTGTCTGCCTGTGACCAAGTTGACTCTGAGGCCCTGGTGGGCTGCC GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC TGTCTTCGCTTGTTGTGTCCCCCCATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGA ACTTTGGAGGCAACCCTGACCGTGTCACCATTTTTTGGCGAGTCTGCGGGTGGCACGAGTG GCAACTGGGGCTACCTGGACCAAGTGGCTGCACTACGCTGGGTCCAGCAGAATATCGCCC TCATCCAGTACCGCCTGGGTGTCCTGGGCTTCTTCAGCACTGGAGACAAGCACGCAACCG TGTGTCTACAGGACCTCACCGCAGTGGAGTCAGAGTTTCTTAGCCAGTTCAACATGACCT CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT 295 ĠĠĂĊĊĂĊĂĊĂĊĂĊĠĠĠĠĊĀĠĠŦĠĊŦĠĠĠĠĀĠŦĊŦŦĠŦĊĊĂŤĠŦĠĂĀĠĠĠĊĠĊĊĀĀŦĠĊĊĠ TGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTC TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGA Conservative 19.8%; 0, Score 345.8; DB 3; Pred. No. 3.6e-87; Mismatches 617; Indels 84; Length 2888 Gaps 652 592 1665 532 472 1305 1485 832 1905 772 1845 412 352 2079 2019 712 1785 1725 1605 1365 952 892 5

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TGCAGAAAATGTTAACGCTGCTGATGTTGCCTCCTACATTTGGTGACCTGCTGAGGAAATCCTGAGAAAATGTTAACGCTGCTGATGTTGCCTCCTACATTTGGTGACCTGCTGAGGAAGGA	2080 ĠĂĠĬĠĠĬĠĂĬĠĠĠĠŢĊŢĬĊĊŢĠĊĊĀĠĠĀĊĊĊĊĀĠĠĀĠĊŢĠĊŢĠĊĊĠĀĊŢ 2139 1013 ŢŢĄĄĠĊĄĄŢŢĊĊŢŢĊĊŢŢĊĊŢĠŢĠĀĊŢĊĄĀŢĄĄĊĀĠĠĀŢĠŢŢĠŢĠŢŢĠ	

RESULT 11
HSM806270
LOCUS
DEFINITION
ACCESSION SOURCE ORGANISM VERSION KEYWORDS COMMENT REFERENCE CONSRTM TITLE JOURNAL AUTHORS Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of th Direct Submission Submitted (22-SEP-2004) MIPS, Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium Homo sapiens HTC Homo sapiens mRNA; cDNA BX538086 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; BX538086.1 Homo sapiens (human) HSM806270 (bases 1 to 3909) GI:31874222 3909 bp mRNA 1 DKFZp686H0466 (from Ingolstaedter Landstr.1, linear HTC 22-SEP-20 n clone DKFZp686H0466). Weil, B., Amid, C Euteleostomi; HTC 22-SEP-2004 D-85764

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GAGTGGTTGATGGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCAT 1012

This clone (DKFZp686H0466) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany

Germany

the

German Genome Project

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Best Local Similarity 54.7
Matches 849; Conservative
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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686H0466
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
TCATCCAGTACCGCCTGGGTGTCCTGGGCTTCTTCAGCACTGGAGACAAGCACGCAACCG
                                        TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGG
                                                                                                                                                                                                  GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGATCCACGGTGGTGCGCTTGTTTTTG
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MASLYDGSMLAALENVVVIIQYRLGVLGFPSTGOKHATGNWGYLDQVAALRWVQQNI
AHFGGNEDRVTIIFGESAGGTSVSSLVVSPISQGLFHGAHMSGYLLPQLIASSADVI
STVANILSACDQVDSBALVGCLRGKSKEBILAINKPFKMIPGVVDGVFFLPRHPQELLA
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LKNIRPHMKADHVKTTEBEEQLSRKMKKYWANFARNGNPNGEGLPHWPLFDQBEQYL
RLNLQPAVGRALKAHRLQFWKKALPQKIQEEBBEERHTEL"
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/clone_Tib="686 (synonym: hlcc3). Vector pSport1_Sfi,
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
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/db_xref="RZPD:DKFZp686H0466"
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Lam. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)

Contact: Shultz MA

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Fax: 530 752 4698

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Average Phred score is 20 or better. All
20) and vector/linker sequence has been r
High quality sequence stop: 1918.
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Mammalia; Eutheria;
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/dev stage="adult"
/dev stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/clone="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                              TTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGGACGAGGAGGAGGAGGAGTTACTGAGC
                                                                                                      AAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCC
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Contact: MGC help deek
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.g Series: IRAK Plate: 42 Row: p Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                             passed the following identity to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Guntratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowie, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2038 bp
Mus musculus, clone IMAGE:5123923,
EC019926
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                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:5123923"
/tissue_type="Liver, normal.
/clone_Tib="NCI_CGAP_Li9"
/lab_host="DH10B"
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986 925 926 871 966 811 806

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                                                                                                                                                    Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1826)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                  Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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full-length cDNA clone CS0DE014YC12
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODE014YC12"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY Cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
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Tetraodon nigroviridis
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/mol_type="mRNA"
/db xref="taxon:99883"
/tissue_type="Liver"
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 AGGGTCTTGTCCACTGGCCAAAGTATGGAGAAACGGAGGAGTACCT
                                                                                      TGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGA 1528
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                                                         TGACCCAAATCATGATGAGCTACTGGGGCAACTTTGCTCGCACAGGGTCTCCTAATGGAC
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Search completed: June 15, 2005, 02:39:45
Job time : 5801.46 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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\GGTGCATTACCCGAAA 360	CTACCCTAATTTGTGC 300	CCTGCGATTTACGAAC 240	AAGCCCTGTGCCTGTG 180	NAGGGCCACAGAGGAAC 120 NAGGGCCACAGAGGAAC 120	CCTGATTCTCCAGCCC 60	Length 1746; Indels 0; Gaps 0	Sequence 15541, A Sequence 3, Appli Sequence 2515, Ap Sequence 2516, Ap Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6,

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TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-13-28
PRIOR FILING DATE: 2001-03-28
INUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO
LENGTH: 2158
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Patent No. 6664091
GENERAL INFORMATION:
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Length 965;

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Ang, Jian...

Ma, Yunqing

Yamazaki, Victori...

Ang, Jian...

Ma, Yunqing

Yamazaki, Victori...

Zhan: Wang, Zhiwei

LICANT: Wang, Zhiwei

LICANT: Wang, Dunrui

APPLICANT: Wang, Yonghong

APPLICANT: Ghosh, Reena

APPLICANT: Ghosh, Reena

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: NO. 6783869el Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 803

CURRENT APPLICATION NUMBER: US/09/799,451

CURRENT FILLING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 948

SOFTWARE: Pt. Fenes Version 2.0

SEQ ID NO 155

LENGTH: 965

TYPE: DNA

ORANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

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LOCATION: (128)...(925)

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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
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APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje
APPLICANT: Drmanac, Radoje
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Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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Sequence 3799, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GEI
TITLE OF INVENTION: WITH HUMAN DISEASE, METH
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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US-09-949-016-3799
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; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-555
                                                                                                   FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 555
                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-949-016-555
; Sequence 555, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
Query Match
                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
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APPLICANT: Danks, Mary K.
APPLICANT: Danks, Mary K.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
FRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Datentin Ver. 2.0
SEQ ID NO 27
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
US-09-595-682B-27
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 876; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/09595682B Patent No. 6800483 GENERAL INFORMATION:
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           CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT
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ilarity 56.5%;
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                                                                                                                                                          Score 406.6; DB 4;
Pred. No. 1.2e-117;
0; Mismatches 639;
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                                                                GAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTG
                                                                                                                                  CGGACTCCATGTTTGTGATCCCTGCACTCCAAGTAGCACATTTTCAGTG----TTCCCGGG
                                                                                                         AGTACATTGGGGÁCAATGGGGATCCCCAGACCCTCCAAGCGCAGTTCCAGGAGATGATGG
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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR PRILING DATE: 1998-02-19
PRIOR FILING DATE: 1998-02-19
PRIOR FILING DATE: 1998-02-12
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 20
LENGTH: 1717
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.8%;
Best Local Similarity 54.8%;
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Pred. No. 8.8e-104;
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                                                                            ACGAAGCCGGCTTTTGTCAAAGCCGACCACCACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGT 1410
                                                                                                                                                 GATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGAC
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Sequence 3, Application US/09264737A

Patent No. 6107549

GENERAL INFORMATION:
APPLICANT: Feng, Paul C.C.
APPLICANT: Reng, Paul C.C.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1701
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Best Local Similarity 54.8%;
Matches 866; Conservative
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Pred. No. 5.2e-102;
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                                                                                                                                                           TCGAAGGAGCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTA 1498
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                                                                                   ACTTTGCTAGGAATGGGAATCCCAATGGAGAAGGGCTTCCTCAATGGCCAGCATATGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application Patent No. 6770799 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: BTI-45
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN TITLE OF INVENTION: TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mor, Tsafrir S. APPLICANT: Soreq, Hermona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: human acetylcholinesterase gene optimized for OTHER INFORMATION: expression in plants
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706 ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC
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Arntzen, Charle
Mason, Hugh S.
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                                       GTGGCAGCCTTCGGGGGTGACCCCGACATCAGTGACGCTGTTTGGGGAGAGCGCGGGAGCC
                                                                                                                                                                                                   GTGTCCATGAACTACCGGGTGGGAGCCTTTGGCTTCCTGGCCCTGCCGGGGAGCCGAGAG
                                                                                                                                                                                                                                      GTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC---ACATGGGATCAGCAT
                                                                                                                                                                                                                                                                                                                  TCAGCCTC-----CATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTT
                                                                          ATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCC
                                                                                                                     GCCCCGGGCAATGTGGGTCTCCTGGATCAGAGGCTGGCCCTGCAGTGGGGTGCAGGAGAAC
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55.1%;
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Pred. No. 4.8e-33;
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US-07-732-962A-1
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
TOTAL MICHAEL ACID
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GENERAL INFORMATION:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/07/732,96: FILING DATE: 19910722 CLASSIFICATION: 435
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
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                                 CCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCC
                                                                                                  TTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTAC
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 CCCAACCGTGAGCTGAGCGAGGACTGCCTGTACCTCAACGTGTGGACACCATACCCCCGG
                                                                   GTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGCACCGAGATGTGGAAC
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Pred. No. 5e-33;
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; NAME/KEY:
; LOCATION:
PCT-US92-06106-1
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; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY AV
; TITLE OF INVENTION: ACETYLCHOLINESTI
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
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PCT-US92-06106-1
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                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 3930.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEPAX: (212) 664-0525

TELEPAX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1845 base pairs
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06106
FILING DATE: 19920722
CLASSIFICATION: 435
                                                    MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         TYPE: NUCLEIC ACID STRANDEDNESS: sing TOPOLOGY: linear
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STATE: New York
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                                              SEQ ID NO 1192
LENGTH: 2158
                                                                                                                                                                                                                                                                                                                    Sequence 1192, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Best Local
                                                                                  PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Versio
               ORGANISM: Human
                               TYPE: DNA
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Pred. No. 5e-33;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

FITTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-00

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION SUMBER: 60/231,498

PRIOR APPLICATION SUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 1193
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US-09-949-016-1193
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Best Local Similarity 55.7
Matches 341; Conservative
                                                                                                                                                                                                                                                                                                    Sequence 1193, Application US/09949016 Patent No. 6812339
 TYPE: DNA
ORGANISM: Human
                                LENGTH: 2158
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Pred. No. 5.6e-33;
0; Mismatches 266;
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                                                                                                                            Sequence 5, Application US/08318826A
PARENT NO. 5891725
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Eckstein, Fritz
TITLE OF INVENTION: Synthetic Antisense
TITLE OF INVENTION: Oligodeoxynucleotides and
TITLE OF INVENTION: Containing Them
NUMBER OF SEQUENCES:
OCCURRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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US-08-318-826A-5
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ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                            STREET: 30500 No. 5891
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
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Pred. No. 5.6e-33,
0; Mismatches 260
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GCCTCGGTGGGCATGCACCTGCTGTCCCCGCCCAGCCGGGCCTGTTCCACAGGGCCGTG
                                                                                                          GTGGCAGCCTTCGGGGGTGACCCCGACATCAGTGACGCTGTTTGGGGAGAGCGCGGGAGCC
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-318-826A-5
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2256 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDN HYPOTHETICAL: NO ANTI-SENSE: NO
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REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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STRANDEDNESS: doub
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GCCTCGGTGGGCATGCACCTGCTGTCCCCGCCCAGCCGGGCCTGTTCCACAGGGCCGTG
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                                                                                                                                                          GCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAAC
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                              ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC 765
                                                                GTGGCAGCCTTCGGGGGACCCCGACATCAGTGACGCTGTTTGGGGAGAGCGCGGGAGCCC
                                                                                                                                   GCCCCGGGCAATGTGGGTCTCCTGGATCAGAGGCTGGCCCTGCAGTGGGTGCAGGAGAAC
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ilarity 55.1%;
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3, 4 and 6"
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Pred. No. 5.8e-33;
0; Mismatches 266;
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US-08-370-156-1
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Best Local Similarity 55.1
Matches 341; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KOHN, KENNETH I 30,955
REGISTRATION UNMBER: 9-30
REFERENCE/DOCKET NUMBER: P-30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,156
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2256 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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475 TCAGCCTC-----CAICCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTT 528
                                                                                                                           514
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                                                                                                                                                                                                                                                                                                                              334 CCTGTCTCTGCTTTCCTGGGCATCCCCTTTGCGGAGCCACCCATGGGACCCCGTCGCTTT
                                                                                                                                                                                                                                                                                                                                                               175 CCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCGCTGGGATCCCCTGCGATTT
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E: Michigan
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                                                                                      GATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGC
                                                                                                                                                                                          GTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGCACCGAGATGTGGAAC
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Pred. No. 5.8e-33;
0; Mismatches 266;
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631 GCTTCCTTGGACGTGTACAGTGCCGCTTCTTGGTACAGGCCGAAGAGCTTGCTGCTGCTG 529 GTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCACCACATGGATCAGCAT 585	유 성	유 성	유 성	음 성	<u> </u>	B
GCCTCCTCGTGGACGTGTACGATGGCCGCTTCTTGGTACAGGCCGAGAGGACTGTGCTGGTGCTCTCGTCCAGGACTACGGACTAGGACTATGGTTTCTTCACCACATGGGATCAGCAT	766 931	706 871	646 811	586 751	52 <u>9</u>	631
	ATGGAGAGTGGGGCA 784	ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC 765	ATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGGGAGTCCGCGGGAGCC	GCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTGTTCTTGTCCTGGGTCCAGAAGAAC	GIGGTCGICCAGTACCGGCTAGGAATAITTGGTTTCTTCACCACATGGGATCAGCAT 585	. GCCTCCTCCTTGGACGTGTACGATGGCCGCTTCTTGGTACAGGCCGAGAGGACTGTGCTG 690

Search completed: June 14, 2005, 23:03:36 Job time: 296.702 secs



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Result
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Maximum Match 100%
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Maximum DB
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Abn84302 Human car
Adg89093 Human uro
Abg86169 Novel huma
Aad40574 Human dru
Acn42766 Human dia
Adb62095 Human cDN
Abx72267 Human NOV
Abg86170 Novel hum
Adr19681 Human dru
Add59146 Cat cauxi
Adf59144 Cat cauxi
Adf59144 Cat cauxi
Adf591344 Human car
Abz11273 Human car
Abz11273 Human car
Abd213344 Human car
Abd31218 Human car
Abd3791 Novel hum
Aaf52558 Nucleottid
Aadf52913 Human car
Abd3791 Novel hum
Aaf52558 Nucleottid
Aadf3791 Novel hum
Aaf52558 Nucleottid
Aadf3791 Human car
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23-SEP-2002 (first entry)

ABN84302;

ABN84302 standard; cDNA; 2158

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22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	23.2	23.3	23.3	23.3	23.3	23.3	
3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3776	2101	1748	2484	2191	2191	2191	2191	
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Ada76491	Ada76547	Ada46060	Aca67707	Aca04294	Aca68601	Acd42065	Aca06084	Abx89411	Aca03873	Acd28810	Ab195693	Ab188204	Abk33640	Aas21514	Aaa96341	Aad08405	Aad00680	Abz24055	Aaf21884	Abn97359	Ab163768	Ab162492	Ab162491	
Human PRC	Novel hum	Novel hum	cDNA enco	Human cDN	Novel	Human sec	cDNA enco	DNA encod		Human sec	Human ang	Human PRO	cDNA enco	Human cDN	cDNA enco	Human sec	Human Hyd	CES2		Gene #385	Brea	Colon ade	Colon	- 1

ALIGNMENTS

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RESULT 1
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IID ABN88
XX ABN88
XX ABN8
AC ABN8
XX ABN8
DT 23-S
XX Huma
XX Carb
KW diag
XX Carb
KW diag
XX Carb
COS Homo
XX CT
T CDS
TT CDS
TT mat_
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53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory; diagnosis; gene therapy; gene; ss.
                                                                                                                  WPI; 2002-547936/58.
P-PSDB; ABB79537.
                                                                                                                                                                                                                         Curtis RAJ, Silos-Santiago
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28-MAR-2001; 2001US-0279508P.
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/product= "53010"
/note= "the CDS is also claimed in Claim 1"
/note= "the CDS is also claimed in Claim 1"
/*tag= b
/*tag= b
174    .1838
/*tag= c
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The present nucleotide sequence, the coding region of which is also C claimed, is that of cDNA encoding human 53010, a novel member of the C carboxylesterase family. The invention provides 53010 nucleic acids, cantisense molecules, expression vectors, host cells, transgenic animals, 53010 proteins, fusion proteins, antigenic peptides, anti-53010 cantibodies and methods for detecting the presence of 53010 polypeptides or nucleic acids, of identifying a compound that binds to the 53010 completed, and of modulating the activity of the polypeptide. The 53010 convergence controlling agents for controlling disorders involving aberrant or controlling agents for controlling disorders involving aberrant or controlling agents for carboxylic esters. As 53010 mRNA is highly capression is regulated in some rodent pain models, 53010 molecules can also act as novel diagnostic targets and therapeutic agents for controlling neurological disorders, such as pain-related disorders. A controlling neurological disorders, such as pain-related disorders. A controlling neurological disorders, such as pain-related disorders. A controlling cell involves administering a compound that modulates 53010 cativity or expression. 53010 nucleic acids are also useful in chromosome carrays, for detection of variations or mutations, as surrogate markers and in pharmacocennomics.
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Best Local Similarity
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27-MAR-2003;
08-MAY-2003;
19-MAY-2003;
The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a unlogical disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; (2) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                    Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
                                                                                                                                                                                                                                                                                                Claim 1;
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26-SEP-2003;
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The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC activity of polypeptides of the invention may be described as, CC cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorders inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder (CC cardiovascular disorders, pancreatitis, respiratory disorder, thyerproliferation, systemic autoinmune diseases, byper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, CC developmental diseases, metabolic diseases, sperm dysfunction, thyroid CC cardiovascular diseases, metabolic diseases, sperm dysfunction, thyroid CC cardiovascular diseases, neurological diseases, stroke, angiogenesis, CC cvalation disorders, diseases in the spinal cord, thyroid gland, heart, CC growth abnormalities, and alleviation of precocious puberty. The CC sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's
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19-MAR-2001;
04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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2001US-0260482P.

2001US-0264922P.

2001US-026797P.

2001US-02767988P.

2001US-0276988P.

2001US-0281535P.
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91

Query Match Best Local Similarity Matches 1654; Conserv

Conservative

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94.7%;

Score 1652.8; Pred. No. 0; 0; Mismatches

Sequence 1728

B₽;

367 A; 483 C; 437 G; 441

T; 0 U; B 2; 6;

0 Other;

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CTCCTCCAGCCTTTCTTTTTCTTTTGTGCTCCTTGA
               CTCCTCCAGCCTTTCTTTTTTTTTTTTTGTGCTCCTTGA 1746
                                                                      ATGAGCCTCGGACAGAGACTCAAAGAACCGGGGGGGGGTGGATTTTTTGGACCAGCACCATCCCC
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Human drug metabolising enzyme (DME-10) cDNA
                                                          AAD40574;
                                                                                     AAD40574 standard; cDNA;
                              (first
                              entry)
                                                                                     2232
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Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis; proliferative disorder; arceriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; anaemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; conjunctivitis; glaucoma; cataract; anorexia; metabolic disorder; cytic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10; gene; ss.

sapiens

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CC are selected from autoimmune/inflammatory disorder such as acquired conveitis; a cell proliferative disorder such as acquired conveitis; a cell proliferative disorder such as arteriosclerosis, conveitis; a cell proliferative disorder such as arteriosclerosis, conveitis; a cell proliferative disorder such as arteriosclerosis, conveitis; a cell proliferative disorder such as arteriosclerosis, conveitis; and cancer; a neurological disorder such as conveitions as renal tubular acidosis, epilepsy, consensa; an expection disorder such as are attract; metabolic conveitis; an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic conveitis, and expection as another such as conjunctivitis, glaucoma, cataract; metabolic conveitis, and as another such as conjunctivitis, glaucoma, cataract; metabolic conveitis, and as another such as conjunctivitis, glaucoma, cataract; metabolic conveitis, and as another such as conjunctivitis, glaucoma, cataract; metabolic conveitis, and as another such as conjunctivitis, glaucoma, cataract; metabolic conveitis, and a number of drug screening techniques and to analyse the conveition and another of drug screening techniques and to analyse the conveition and another of drug screening techniques and to analyse the conveition and another conveiting differences in the chromosomal conveition, inversion, etc. among normal, carrier or conveiting defected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10 cDMA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, where the disorders
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Lee EA, Ding L, Ha
Lal PG, Warren BA,
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P-PSDB; AAE25025.
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15-DEC-2000; 2000US-0256189P
21-DEC-2000; 2000US-0257713P
19-JAN-2001; 2001US-0267706P
02-FEB-2001; 2001US-0266020P
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                                                            GGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCT
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BA, Yang J, Walia NK, Nguyen DB, Gandhi
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer Patury S, Shi X, Suarez CJ;
The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated
                                                                                            New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
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12-SEP-2002;
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                                                     GCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA
                                                                                  GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA
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       neurological disease; cancer; tumour.
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Query Match Best Local Sim Matches 1653;

Similarity

93.4%;

Score 1631.2; Pred. No. 0; 0; Mismatches

Conservative

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10;

Gaps

197 210 257

Sequence

2092 BP; 464 A; 552

C; 497

ဂ္ 579

T; 0 U; DB 10; ω,

0 Other; Length 2092;

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The invention discloses a polymucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polymucleotide CC or its partial peptide, a mantibody binding to the polypeptide or peptide of the polymucleotide, immunologically assaying the polypeptide or peptide of peptide of the polymucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polymucleotide in an CC expressible manner and an antisense polymucleotide. The oligonucleotide is as a probe CC for detecting the polymucleotide. The polymucleotide and encoded CC proteins are useful as pharmaceutical agents and many disease-related CC genes may be included in them, for developing a diagnostic marker or CC effects for regulation of their expression and activity, or as targets CC regeneration. Membrane proteins, signal transduction-related proteins, of developing and civity or as targets CC encoding them can be used as indicators for diseases (e.g. osteoporosis, concer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The CC sequence presented is a cDNA of the invention. Note: Some of the sequence is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides and polypeptides, useful for developing marker or medicines for regulation of their expression and
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P-PSDB; ADB64065.
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25-JAN-2002;
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Yoshikawa T,
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                                   CACCATCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCCTTAAC
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ABX72267 standard; CDNA; 1746 ВP

ABX72267;

03-JUN-2003 (first entry.

Human XAON polynucleotide #98

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XX H Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; A hypertension; congenital heart defect; aortic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus pulmonary stenosis; subsortic stenosis; ventricular septal defect; VSD tuberous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease; arteriosus; defect; VSD;

Homo sapiens.

WO200281498-A2

17-OCT-2002

03 APR-2001; 03 APR-2001; 05 APR-2001; 05 APR-2001; 06 APR-2001; 10 APR-2001; 11 APR-2001; 12 APR-2001; 13 APR-2001; 17 APR-2001; 19 APR-2001; 20 APR-2001; 23 APR-2001; 23 APR-2001; 24 APR-2001; 24 APR-2001; 25 APR-2001; 03-APR-2002; 2002WO-US010780.

2001US-0281066P.
2001US-0281163P.
2001US-0281863P.
2001US-0281906P.
2001US-0282930P.
2001US-0282934P.
2001US-02839312P.
2001US-0283712P.
2001US-0283714P.
2001US-0283715P.
2001US-0285385P.
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22-MAY-2001;
29-MAY-2001;
30-MAY-2001;
18-JUN-2001;
19-JUN-2001;
12-SEP-2001;
25-SEP-2001;
25-SEP-2001;
25-SEP-2001;
17-OCT-2001;
14-NOV-2001;
16-JAN-2002;
16-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD; Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach V Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman K;
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                                                                                                                                                                                                                                                                                                                  Similarity
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                                                   CTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTG
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trachea; thymus; lymph node; muscular system; obesity; anorexia;
growth abnormality; precocious puberty; gene; ss.
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SMITHKLINE
GLAXO GROUP
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2001US-0264922P.
2001US-0266797P.
2001US-0276988P.
2001US-0281535P.
2001US-0289622P.
  Birkeland M,
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Cogswell JP, Kabnick
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-508784/54.
P-PSDB; ABP61005.
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Pred. No. 0;
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                                              TACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGGTGGAT
                                                                                                                                                         ACGGAGGAGGAGTTACTGAGCCGGAAGATGATGAATACTGGGCTACCTTTGCTCGA
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                             TACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGAGAGAT
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Azimzai Y, Elliott VS, Lal P, Lee Ring HZ, Sa Walsh RT, W Human drug metabolizing enzymes, useful idisorders associated with aberrant (DME) autoimmune disorders. P-PSDB; 2002-362498/39. DB; ADR19663. ii Y, Baughin MR, But VS, Gandhi AR, G.
Lee EA, Lu DAM, I
IZ, Sanjanwala MS, YRT, Warren BA, Xu Borowsky ML, Ding L, Duggan BM; Griffin JA, Hafalia AJA, Ison CH, K Nguyen DB, Arvizu C, Policky JL, R, Tang YT, Tribouley CM, Narinder WK; u Y, Yang J, Yao MG, Yue H; in the diagnosis and treatment activity, e.g., cancer and Khan Ramkumar ဓ္ဌ 4

INC.

Claim 12; SEQ ID NO 20; 142pp; English.

This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a gene which encodes a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.

1857 BP; 428 A; 487 Ç Ģ 446 7, 0 ₽ 0

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P-PSDB; ADA54807.
                                                                                                         Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                                                    cat kidney disease marker;
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                                                                                                                                                                                                                                                                                                               CDNA;
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The present sequence encodes a cat cauxin protein (I) or its salt, which CC is cat kidney disease marker. Also described: (I) a partial peptide (II) cof (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) CC comprising (III); (4) a transformed host (V) comprising (III) or (IV); (CC comprising (III) or (II) by culturing (V); (6) a antibody (VI) which CC couples specifically with (I) or (II); (7) diagnosing cat kidney disease CC which involves measuring (I) quantitatively, and where reduction of CC amount of (I) indicates presence of the disease; (8) a cat kidney disease CC diagnostic agent comprising (I) labelling agent, a reagent which measures CC the biological activity of urinary (I) or (VI); and (9) a cauxin CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney CC disease. (I) provides an early marker for the disease, and replaces CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1329; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2145 BP; 444 A; 581 C; 550 G; 564 T; 0
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Matches 1265; Conserv
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                                                                             AGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTGCTTTGAA 1347
                                                                                                                            CTGGACTTGCTTGGAGATGTGCTCTTTGTGGTCCCTGGGGTGGTCACAGCTCGATATCAT 1260
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RESULT 13.
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                                                                                                                                                                                    19-DEC-2000;
20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
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(SMIK )
(GLAX )
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    Agarwal
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04-APR-2001;
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                                                                                                                          2000US-0257048P.
2001US-0260482P.
2001US-026492P.
2001US-0266797P.
2001US-0276988P.
2001US-0276988P.
2001US-0281535P.
2001US-0289622P.
    Birkeland M,
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                                             GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precocious puberty; gene; ss.
    Cogswell JP,
                                                                  CORP
      Kabnick KF,
      Lai
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Matches 1022; Conservative
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      CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT 1263
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Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                Martensen SA,
                                                                                                                                                                                   Smith RF,
                                                                                                                                                                                   Strum
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                                                                                                                                                                                   Xie
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       disorder
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CC cytostatic, vulnerary, antiparteriosclerotic, antiparkinsonian, nootropic, CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, CC and metabolic. Polypeptides and polymucleotides of the invention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease CC and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, CC inflammation, neoplastic diseases, nervous system related disorders and CC cardiovascular disorders, pancreatitis, respiratory disorder, CC hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, CC developmental diseases, metabolic diseases, sperm dysfunction, thyroid CC disorders e.g. hypothyroidism, brain damages, colitis, cone photoculation deficiency, neurological diseases, stroke, angiogenesis, CC covulation disorders, diseases in the spinal cord, thyroid gland, heart, CC crachea, thymus, lymph node and muscular system, obesity, anorexia, CC growth abnormalities, and alleviation of precocious puberty. The The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's

Sequence 1071 BP; 242 A; 286 C; 254 G; 289 T; 0 U; 0 Other;

CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC CCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCCTCCATCTGATACAAAACATCCTG CCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCT GGTGCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATT GGTGCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATT CCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGAT CATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAA ATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCA ATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCC ATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCC CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC CCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAACATCCTG CCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGAT CATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAA 58.5%; Score 1021.4; DB 6 99.9%; Pred. No. 5.5e-291; tive 0; Mismatches 1; DB 6; Indels Length 1071 0, Gaps 1143 1023 1203 468 408 1083 348 288 963 903 168 843 108 783 528 228 0

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WPI; 2003-269506/27.
P-PSDB; ADC55524.
                         Mao Y,
                                                        26-APR-2001; 2001CN-00112736
                                                                        26-APR-2001; 2001CN-00112736
                                                                                         04-DEC-2002
                                                                                                         CN1382799-A
                                                                                                                                                                      human carboxylatase-24.64; primary hypertension; nephrotic; bronchial asthma; gene; ss.
                                                                                                                                                                                              Human carboxylatase 24.64 encoding sequence
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                                         BIOWINDOW GENE DEV INC SHANGHAI
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Claim 6; SEQ ID NO 1; 31pp; Chinese.
                                                              Polypeptide-human carboxylatase-24.64 and
                                                              polynucleotide
                                                              for
                                                             coding
                                                              it.
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The present invention relates to a polypeptide-human carboxylatase-24.64, the polynucleotide for coding it, the process for preparing the polypeptide by DNA recombination, the application of the polypeptide in treating diseases such as primary hypertension, digestive ulcer, nephrotic, bronchial asthma, tremor, etc., the antagon of the polypeptide and its medical action, and the application of the polynucleotide are new. The present sequence represents human carboxylatase 24.64 encoding

Sequence 1244 BP; 301 A; 314 C; 271 G; 358 T; 0 U; 0 Other;

Query Match

Similarity

51.8%; 99.7%;

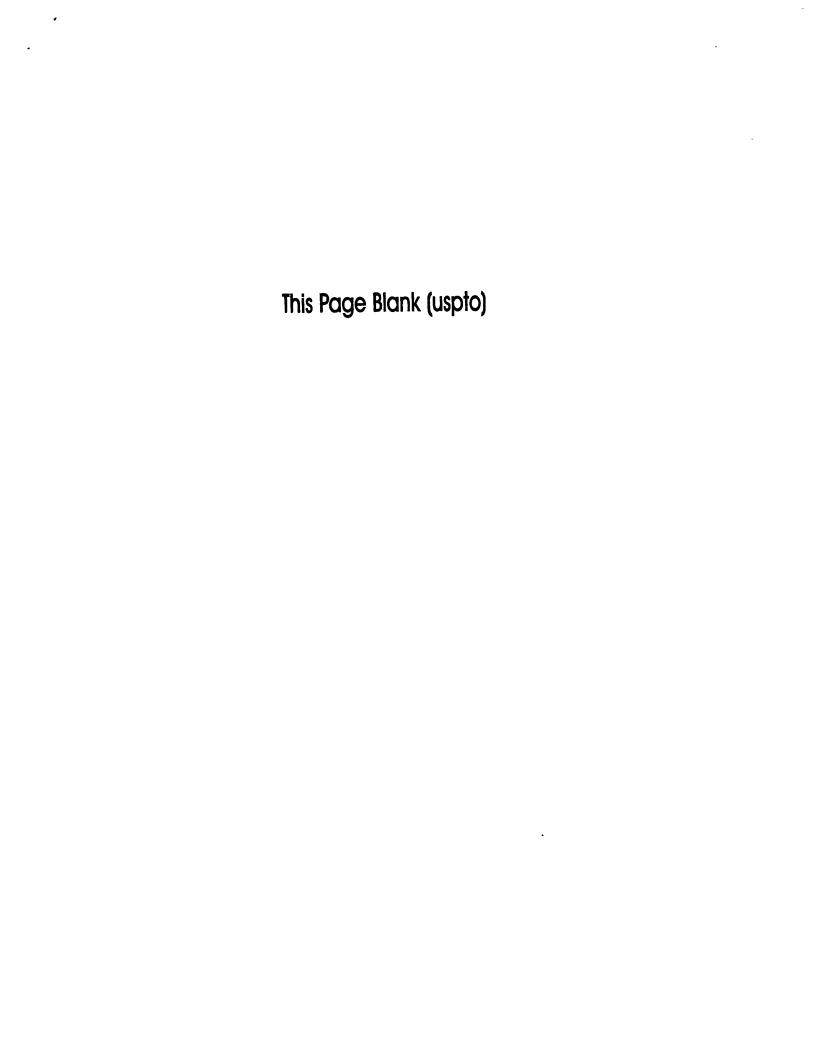
Length

밁 S δ 밁 S 밁 δ В S 밁 8 밁 S 밁 S 밁 δ 밁 Ś á 밁 밁 S 밁 Ş 밁 S Best Local Sim Matches 907; 1617 1497 1437 1377 1317 1257 1137 1077 1017 721 601 541 481 421 361 301 241 181 121 957 897 837 61 ACCGCGGGTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCT 1676 TACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAA GTTCGAAGGAGCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGC 1496 TCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGA 1616 TACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAA 1556 GTTCGAAGGAGCCACGAGGAGGAGGAGTTACTGAGCCGGAAGATGATGAAATACTGGGC CCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTAT CCACGCTGATGAAGTCCGCTTTGTGTTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTAT TGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCAGCTTTTGTCAAAGCCGA TGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGA GGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTA 1316 AGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCTATGAA 1076 GGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAG GGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGCTGCTACCTGCTACTTCTA CATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAA CATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAA GGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAA GACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGT GACAAAACCTTCCAAGGAGCTGCTGAGCCTCAGCCAGAAAACAAAGTCTTTTCACTCGAGT GGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAA GGTTGATGGTGCTTTCCTTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAA 1016 GGTTGATGGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAA GETTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAG Conservative Score 905.2; DB 10; Pred. No. 1.4e-256; 0; Mismatches 3; Indels 0 Gaps 1436 540 1376 780 720 660 600 480 1256 1196 1136 420 360 300 180 60 120 956 0

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disease, such as organophosphorus intoxication, cancer and osteoporosis. Compounds that increase the ability of human carboxylesterase-like enzyme to bind to organophosphorus compounds are useful as detoxifying agents. Carboxylesterase-like enzyme agonists and antagonists are useful for treating osteoporosis, Paget's disease and degradation of bone implants, particularly dental implants. Carboxylesterase-like enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the nucleic acid sequences which encode the enzyme. The coding sequence of carboxylesterase-like enzyme polynucleotide is useful in gene therapy and for generating antisense oligonucleotides or ribozymes which specifically bind to mRNA transcribed from carboxylesterase-like enzyme DNA. These antisense oligonucleotides are
                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a purified human carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme and its DNA are useful for screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme useful for treating a carboxylesterase-like enzyme dysfunction related useful for treating a carboxylesterase-like enzyme dysfunction related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 4; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication,
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Matches 743
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                                                         TCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGGTCCCTGCACTGATCA 1273
                                                                                                      TCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCC 1093
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                                           TCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGATCCCTAAGCTGATCA
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Search completed: June 14, 2005, 18:10:11 Job time: 944.402 secs



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-Q=/Cgn2 1/USPTO spool/6664091/runat 14062005 133458 9325/app query.fasta 1.4238
-DB=A Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=664091 @CGN 1 299 @runat 14062005 133458 9325 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

Human carboxylesterase family member 53010

23-SEP-2002 ABB79537;

(first entry)

ABB79537 standard; protein;

581 AA

Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory;

diagnosis; therapy.

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RESULT 1
ABB79537
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence of human 53010, a novel CC protein containing the structural characteristics of a carboxylesterase CC family member. The invention provides 53010 nucleic acids, antisense CC molecules, expression vectors, host cells, transgenic animals, 53010 CC proteins, fusion proteins, antigenic peptides, anti-53010 antibodies and CC methods for detecting the presence of 53010 polypeptides or nucleic acids, of identifying a compound that binds to the 53010 polypeptide, and CC controlling the activity of the polypeptide. The 53010 polypeptide and CC nucleic acids can act as novel diagnostic and therapeutic agents for CC controlling disorders involving aberrant or deficient hydrolysis of CC carboxylic esters. As 53010 mRNA is highly expressed in the central and CC pain models, 53010 molecules can also act as novel diagnostic targets and CC therapeutic agents for controlling neurological disorders, such as pain-CC (especially a pain-related disorder) characterised by aberrant activity of a 53010 expressing cell involves administering a compound that CC modulates 53010 activity or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as surrogate markers, in tissue typing and chromosome mapping.
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28-MAR-2001; 2001US-0279508P.
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                                                  CTCCAGAACTCAGAGTGGCTGCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAA
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                                     LeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLys
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The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological
                                                                                                                                      Use of polypeptides related to urological disorders, e.g. 44390, 5. 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological disorder.
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RESULT 3
ABP61004
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wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; typerproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colicis; cone photo- transdauction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; trachea; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
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Homo

growth abnormality;

precocious puberty

WO200250105-A1

27-JUN-2002

17-DEC-2001; 2001WO-US049232

19-DEC-2000; 2000US-0256710P.
20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0266492P.
30-JAN-2001; 2001US-0266492P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-027698B.
04-APR-2001; 2001US-0281535P.
08-MAY-2001; 2001US-0289622P.

(SMIK) SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC. GLAXO GROUP LTD.

Agarwal P, SA, Birkeland M, A, Rizvi SK, Cogswell JP, Kabnick KF, Smith RF, Strum JC, Xie Ö

N-PSDB; WPI; 2002-508784/54. DB; ABQ86169.

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.

Claim 1(a); Page 312-313; 335pp; English.

CC The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC activity of polypeptides of the invention may be described as, cotypostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, CC neuroprotective, immunosuppressive, heemostatic, antiparkinsonian, nootropic, CC cardiant, antiulcer, virucide, antityroid, cerebroprotective, anorectic, cardiant, antiulcer, virucide, antityroid, cerebroprotective, anorectic, CC useful in the treatment, or as a vaccine in the prevention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and CC cardiovascular disorders, pancreatitis, respiratory disorders, thyperproliferation, systemic autoimmune disease, hyper-immunity, CC haematological diseases, mervous system related content, thyroid developmental abnormality, gastrointestinal ulceration, neuropathy, cancers experimental diseases, mervous system related the property of the cardiovascular diseases, mervous system related disorders, and cardiovascular diseases, mervous system related disorders, thyperproliferation, systemic autoimmune disease, hyper-immunity, cc developmental abnormality, gastrointestinal ulceration, neuropathy, that disorders e.g. hypothyroidism, brain damages, colitis, cone photo-

F

ABP61004 standard;

protein; 575

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97.02%
91.96%
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 4
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Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis;
                 Human drug metabolising enzyme (DME-10).
                               30-OCT-2002
                                           AAE25025;
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GAGGCCCTGCTGAGGTGCCTGAGGACAAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAG
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proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; anaemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epileps; thrombosis; peptic ulcer; anorexia; metabolic disorder; eyetic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10.

Homo sapiens.

WO200246426-A2 Domain Domain Domain Domain Domain Peptide /note= note= 113. .135 /label= Signal_peptide 32. .56 Location/Qualifiers note= note= 'note= 'note= .642 . 250 .314 "Transmembrane domain" "Transmembrane "Transmembrane "Transmembrane "Transmembrane "Transmembrane domain" "Mature human DME-10" domain" domain" domain" domain"

13-JUN-2002.

04-DEC-2001; 2001WO-US047429

2000US-0254308P

08-DEC-2000; 15-DEC-2000; 21-DEC-2000; 19-JAN-2001; ; 2000US-0256189P. ; 2000US-0257713P. ; 2001US-0262706P. ; 2001US-0266020P.

(INCY-) INCYTE GENOMICS INC.

Lee EA, Lal PG, Ison CH; Sanjanwala MM, la MM, Yao MG, Au-Young J, Baughn MR, Arvizu C, Ding L, Hafalia AJA, Tang YT, Yue H, Tribouley Warren BA, Yang J, Walla NK, Nguyen DB, Gandhi Ring HZ; CM, Lu D; AR, Lu Y

2002-519668/55. DB; AAD40574.

Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal

Claim 65; Page 155-156; 169pp; English.

The invention relates to an isolated human drug metabolising enzyme (DME)
CC and its nucleotide. DME is useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of DME, where the disorders
CC are selected from autoimmune/inflammatory disorder such as acquired
CC unventis; a cell proliferative disorder such as arteriosclerosis,
CC cirrhosis, hepatitis, and cancer; a neurological disorder such as
CC Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections
CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections
CC is ne eye disorder such as conjunctivitis, glaucoma, cataract; metabolic
CC disorder such as anorexia, peptic ulcer; and liver disorders. DME is
CC useful in a number of drug screening techniques and to analyse the
CC proteome of a tissue or cell type. The invention is useful for creating

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Ş	g Qy	B 8	B &	B 8	QQ dd	D Q	D Q	р Q	p Q	Db Qy	B 8	dg dg	dg Vy	US-10-	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	88888888888888888888888888888888888888
871 TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGC 930	811 TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC 870 	751 TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT 810	691 GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA 750	631 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC 690 	571 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC 630	511 TATGAGGACGTGCTGGTGGTCGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC 570	451 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 510	391 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC 450 	331 CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG 390 	271 CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 330 	211 CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270 	151 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT 210	91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATTGAATTCAGGGCAAGCAA	-023-515-3 (1-1746) x AAE25025 (1-642)	nment Scores: . No.:	knock-in humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10 Sequence 642 AA;

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RESULT 5
ABM8 4114
ABM8 4114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel diagnostic and therapeutic polynucleotides considered from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorders, developmental disorder, endocrine CC disorder, neurological disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the printed specification, but was obtained in electronic format directly cc from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer
Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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N-PSDB; ACN42766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC extractic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polymucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease and polymucleotides, harkinson's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular diseases, pancreatitis, respiratory disorder, hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, haematological diseases, metabolic diseases, stroke, angiogenesis, CC developmental abnormality, brain damages, colitis, cone phototransduction deficiency, neurological diseases, stroke, angiogenesis, CC valation disorders, diseases in the spinal cord, thyroid gland, heart, CC trachea, thymus, lymph node and muscular system, obesity; anorexia, CC trachea, thymus, lymph node and muscular system, obesity; anorexia, CC proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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                        GAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACC 1512
                                                           CGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACG 1452
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                                                                                                                        CCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTC
                                                                                                                                                                    ACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGG
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. 8	Query DB: US-10-	Pred. No Score: Percent Best Loc	SQ Alig	\$8888	នេងន	rg r r	X R R X	PI	X P P	X R R	3 X # X	XZ	28×	222	XXX	S F	aŭ	RESULT ADA548	문	Ş	B &	B B	S
GGTGCTTTTTCCTGATTCTCC	Match: 82.21% Indels: 6 Gaps: ·023-515-3 (1-1746) x ADA54807 (1-525)	1.26e-241 2606.00 milarity: 88.77% Similarity: 88.25%	SQ Sequence 525 AA; Alignment Scores:	proteins (ADA59707-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.	Claim 14; SEQ ID NO 2375; 205pp; English. The present invention relates to novel human secretory or membrane	New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.	03-395539/38. ADA53168.	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S; Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;	(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.	14-SEP-2001; 2001JP-00328381. 24-JAN-2002; 2002US-0350435P.	19-MAR-2003. 21-MAR-2002; 2002EP-00006586.	EP1293569-A2.	Homo sapiens.	Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.	Human protein, SEQ ID 2375.	20-NOV-2003 (first entry)	ADA54807;		546 TrpValThrGlyTyrPro 551	1633 TGGACCAGCACCATCCCC 1650	1573 CTCCAGCTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTT 1632		1513 GGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGA
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; 2001US-0281863P.
; 2001US-0281906P.
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Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD; Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlaci Padigaru M, Shimkets RA, Gangolli EA, Taupler RJ, Casman SJ, Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; ~ ¥ .

N-PSDB; WPI; 2003-046858/04. ABX72267.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 1; Page 303; 666pp; English

The invention relates to human polypeptides, termed NOVX, and the polypurcleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, actic tenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides invention

Sequence 581

Score:
Percent Similarity:
Best Local Similarity: Alignment S Pred. No.: Scores: 8.79e-241 2597.50 95.07% 94.31% Length:
Matches:
Conservative:
Mismatches: 581 497 4

Query DB:

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                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Azimzai Y,
Elliott VS
Lal P, Le
Ring HZ,
Walsh RT,
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tt VS, Gandhi AR, G
Lee EA, Lu DAM, II
IZ, Sanjanwala MS, I
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                                                         ArgGluAlaThrSerTyrProABnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp
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  TATGAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC 570
                 GENOMICS
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2588.50
94.62%
94.42%
81.66%
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Griffin JA, Hafalla AJA, Ison CH, K
Nguyen DB, Arvizu C, Policky JL, R
Tang YT, Tribouley CM, Narinder WK;
u Y, Yang J, Yao MG, Yue H;
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Ramkumar
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ATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCC 1650
                                                                   GACTIGCTTGGAGAIGIGTTCTITGTGGICCCIGCACTGAICACAGCTCGAIATCACAGA 1290
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                                                                                                            AlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeu
                                                                                                                                 GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTACTG 1470
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Alignment Scores: 
Pred. No.:
                                                                              The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel control of the polynucleotide. Also claimed is a polypeptide encoded by the polynucleotide or peptide or peptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding compared the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe contacting the polynucleotide and encoded control of the polynucleotide and encoded control of the polynucleotide in the proteins are useful as pharmaceutical agents and many disease-related control of their expression and activity, or as targets of genes may be included in them, for developing a diagnostic marker or confidence therapy. The genes are involved in tissue and/or cell confidence therapy. The genes are involved in tissue and/or cell concording them can be used as indicators for diseases (e.g. osteoporosis, encoding them can be used as indicators for diseases (e.g. osteoporosis, concurological disease, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed concern parent office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Suy-, Yamamoto J, Isono Y
                                                 Sequence 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-450961/43.
N-PSDB; ADB62095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related prottranscription-related protein; osteoporosis; neurological disease;
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25-JAN-2002; 2002US-00350978.
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T, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai K, Ix
Otsuka M, Nagahari K, Masuho
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    Length:
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K, Irie
Masuho Y;
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                                                                                                AATGAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTG
                                                                                                                                                       GCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCT 1176
                                                                                                                                                                                               GlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSerLeu
                                                                                                                                                                                                                                                      GGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAG 1356
                                              CTTGGAGATGTGTTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCT 1296
                                                                                AsnGluTyrPheHisAspLysHisSerLeuThrGluIleArgAspSerLeuLeuAspLeu
                                                                                                                                          AlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeuValAla
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The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (I) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosting cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin
                                                                                                                                                                                                                                                                                                                        Felis catus
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                                                                                                                                          cauxin protein or its salt, useful as or diagnosing cat kidney disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection kit which measures cauxin in a test sample. (I) is useful as a cat kidney disease marker and (VI) is useful for diagnosing cat kidney disease. (I) enables detection of cat kidney disease simply and correctly. (I) provides an early marker for the disease, and replaces complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, blood testing.
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                                GlyAspGluArgLysLysAspLeuGlnValLeuAlaArgIleCysGlyCysHisAlaSer
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                                                                                                                                                                                                                                                                                                                cat kidney disease marker; kidney disease
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which is cat kidney disease marker. Also described: (1) a partial peptide (II) (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosing cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin detection kit which measures cauxin in a test sample. (I) is useful as a cat kidney disease marker and (VI) is useful for diagnosing cat kidney disease. (I) enables detection of cat kidney disease, and replaces complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, block testing
Sequence 542 AA;
                                        blood testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-002277/01.
N-PSDB; ADF50146.
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a cat cauxin protein (I) or its salt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as a cat kidney disease marker,
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Query Match:

Percent Similarity: Best Local Similarity:

US-10-023-515-3 (1-1746) x ADF50147

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                                                                                                     GluGlyValProLeuTrpProAlaTyrThrGlnSerGluGlnTyrLeuLysLeuAspLeu
                                                                                                                 AACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTG
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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart trachea; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty.
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GLAXO GROUP LTD.
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heart;

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder

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Claim 1(a); Page 315; 335pp; English.

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ABP61006

standard;

protein;

The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cycostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, amorectic, and metabolic. Polypeptides and polymucleotides of the invention are wound healing disorders, infection, atherosclerosis, Parkinson's disease, command healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, paper laminativ, pastrointestinal ulceration, neuropathy. CC haematological diseases, metabolic diseases, hyper-lamunition, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photocransduction deficiency, neurological diseases, stroke, angiogenesis,

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                                                     GGAGCCACGGAGGAGGAGTTACTGAGCCGGAAGATGATGATAATACTGGGCTACCTTT
                                                                                     AspGluValArgPheValPheGlyGlyAlaPheLeuLyBGlyAspIleValMetPheGlu
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                                                                               The invention relates to a purified human carboxylesterase-like enzyme control of the invention relates to a purified human carboxylesterase-like enzyme and its DNA are useful for screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme is carboxylesterase-like enzyme is useful for treating a carboxylesterase-like enzyme dysfunction related control of the compounds that increase the ability of human carboxylesterase-like enzyme to bind to organophosphorus compounds are useful as detoxifying agents. Carboxylesterase-like enzyme agonists and antagonists are useful for treating osteoporosis, Paget's disease and degradation of bone implants, carboxylesterase-like enzyme is useful in diagnostic assays for detecting disease and degradation of bone implants, carboxylesterase-like enzyme is useful in control of the presence of compounds in the nucleic acid sequences which encode the enzyme. The coding sequence of carboxylesterase-like enzyme polynucleotide is useful in gene therapy and for generating antisense oligonucleotides or carboxylesterase-like enzyme specifically bind to mRNA transcribed from carboxylesterase-like enzyme gene expression. The present sequence is rat carboxylesterase-like enzyme expression. The correspondence is rat carboxylesterase-like enzyme expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication, cancer and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteopathic; gene therapy; osteoporosis; antisense therapy; cy detoxifying agent; Paget's disease; bone implant degradation; dental implant; enzyme; gene expression.
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                                                                                               ATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAAGAGTGAG
                                                                                                                                                                     ATCGAGTTCTTCGGTGGGGACCCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCC
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                     CTGAGGTGCCTGAGGACAAAACCCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAAACAAAG
                                          ThrValSerThrThrValAlaLysLeuSerGlyCysGluAlaMetAspSerGluAlaLeu
                                                               GACCTGCAG----GTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTG
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                  Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuler; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple solerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
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                                                                               GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMetLysAlaAsp
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Search completed: June 15, 2005, 08:41:33 Job time : 155.014 secs	1618 CCGCGGGTGGATTTTTGGACCAGCACCATCCCC 1650 ::: 523 HisArgLeuGlnPheTrpLysLysAlaLeuPro 533	1558 CTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGAGACTCAAAGAA 1617 	1498 ACCTTTGCTCGAACCGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAAT 1557	1438 TTCGAAGGAGCCACGAGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCT 1497



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Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/664091/runat_14062005_133459_9346/app_query.fasta_1.4238
-DB=PIR 79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.I. LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bibosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MUN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=664091_@CGN 1 1.011 @runat_14062005_133459_9346 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY-NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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thiolesterase B (BC 3.....) precursor - mallard C;Species: Anas platyrhynchos (mallard) C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_c;C;Accession: A47162 R;Hwang, C.S.; Kolattukudy, P.E. J. Biol. Chem. 268, 14278-14284, 1993 A;Reference number: A47162; MUID:93300823; PMID:8314791 A;Accession: A47162; MUID:93300823; PMID:8314791 A;Accession: A47162 Ś A;Cross-references: UNIPROT:Q04791; GB:L05493; NID:g213100; PIDN:AAA49223.1; PID:g213101 C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: hydrolase 밁 밁 5 Percent Similarity: Best Local Similarity: A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-557 <HWA> US-10-023-515-3 (1-1746) x A47162 (1-557) Pred. No.: Alignment Scores: F;56-545/Domain: cholinesterase homology <CHE> Query Match: Score: 208 GCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAAC 148 CAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCT 43 23 ThrGlyGlnLysAlaGluGlnProGluValValThrAsnTyrGlySerValArgGlyTyr 42 GlnValLysValAsnAlaAlaGluArgSerValAsnValPheLeuGlyLeuProPheAla 1298.50 62.77% 48.36% 40.96% 2 1.99e-92 Conservative: Mismatches: Indels: Length: Matches: 05-May-1995 #text_change 09-Jul-2004 Gaps: 557 265 79 177 27 Œ CDNA and stimulation of expre 267 207 62

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                                                            IleGlyValAlaGluAsnArgAlaGlnValArgAspGlyLeuLeuAspSerIleAlaAsp
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A34329
60K esterase (EC 3.1.1.-) isoform 2 - rabbit
65K esterase (EC 3.1.1.-) isoform 2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34329
R;Ozols, J.
J. Biol. Chem. 264, 12533-12545, 1989
A;Title: Isolation, properties, and the complete amino acid sequence of a financial sequence of a financial sequence number: A34329; MUID:89308686; PMID:2745458
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Best Local Similarity:
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C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
E;32-517/Domain: cholinesterase homology <CHE>
                                                                                                                                                                                                                                                                        US-10-023-515-3 (1-1746) x A34329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;32-517/Domain: cholinesterase homology <CHE>F;201,430/Active site: Ser, His #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-532 <OZO>
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                                                                                                                 AspAlaGlyValHisThrPheLeuGlyIleProPheAlaLysProProLeuGlyProLeu
CCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTG
                                    ArgPheAlaProProGluProAlaGluAlaTrpSerGlyValArgAspGlyThrSerLeu
                                                                          CGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTAC
                                                                                                                                                         CCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCGCTGGGATCCCTG
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Conservative:
Mismatches:
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CTGACTGAAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT
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                                                                          GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT
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(C,Species: Homo sapiens (man)
(C,Species: Homo sapiens (man)
(C,Date: 10.6sp.199) #sequence_revision 10.5sp.1999 #text_change 09-Jul-2004
(C,Accession: JC5408
(R,Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 23, 117-120, 1997
A; Fitle: Molecular cloning and characterization of a novel putative carboxylesterase, preparation in the commun. 23, 117-120, 1997
A; Rocession: JC5408; MUID:97289502; PMID:9144407
A; Accession: JC5408
A; Molecula type: many
A; Accession: JC5408
A; Molecula type: many
A; Cross-references: UNIPROT:000748; GB:Y09616; NID:g2058317; PIDN:CAA70831.1; PID:g205831
A; Experimental source: intestine
C; Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters &
                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; glycoprotein E;58-944/Domain: cholinesterase homology <CHB>
F;15-95,132-280,291-428/Disulfide bonds: #status predicted F;111,276/Binding site: carbohydrate (Asn) (covalent) #status F;228,457/Active site: Ser, His #status predicted
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JC5408
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A;Gene: GDB:CES2; iCE; CE2
A;Cross-references: GDB:99
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                                                                                        CCCCCCCTGCGATCTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG
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|GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMetLysAlaAsp
                                                                       IleProAlaLeuGlnValAlaHisPhe---GlnCysSerArgAlaProValTyrPheTyr
                                                                                           GTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTAT 1317
                                                                                                                                            {\tt GlyAspProGlnThrLeuGlnAlaGlnPheGlnGluMetMetAlaAspSerMetPheValue}
                                                                                                                                                                                                                                                  ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG
                                                                                                                                                                                                                                                                                                                    GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCCATCTGATACAAAAC 1137
                                                                                                                                                                                                                                                                                                                                                    ATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT------ATGAAG 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGITTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                                                                                               AspThrGlnLysGluMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr 377
                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-561 <SON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carboxylesterase (EC 3.1.1.1) precursor - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change C;Accession: $47655 R;Sone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y. Blochim. Blophys. Acta 1207, 138-142, 1994 A;Title: Cloning and sequence analysis of a hamster liver cDNA e; A;Reference number: $47655; MUID:94318665; PMID:8043605 A;Accession: $47655
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AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC
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                                                 SerLysGluArgLysIleIleLeuProThrIleSerMetSerGluAspCysLeuTyrLeu
                                                                   CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
                                                                                                                  ArgAspGlyThrSerGluProAlaMetCysLeuGlnThrAspPheMetArgProGlnIle 105
                                                                                                                                            CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT
                                                                                                                                                                                      HisArgLeuGlnPheTrpLysLysAlaLeuPro
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GluLeuLeuAlaSerValAspPheHisProValProSerIleIleGLyValAspSerAsp 344
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                                                                                 CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTC-----CTGAAGGGGGACATT 143:
                                                                                                                                                                CGGCACCGGCCTCAGTGCTTT-----GAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                                                                                                                 GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT 132:
                                                                                                                                                                                                                                                        ProGlnThrLeuGlnAlaGlnPheArgGluLeuMetLysAspPheMetPheValllePro
                                                                                                                                                                                                                                                                                     CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT 126:
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GluCysGlyTrpGlyValProLeuPheMetGlyLeuAspHisValIleLysAsnIleThr 364
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                                                               HisGlyAspHisValAlaPheValPheGlySerAspPheTrpGlyLeuLysIleAspLeu
ThrGluGluLysLeuLeuAsnLysArgMetMetLysTyr
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carboxylesterase (EC 3.1.1.1) - mouse C.Species: Mus musculus (house mouse) C; Species: Nus musculus (house mouse) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Accession: S34607 R; Aida, K.; Moore, R.; Negishi, M. Biochim. Biophys. Acta 1174, 72-74, 1993 Biochim. Biophys. Acta 1174, 72-74, 1993 A; Reference number: S34607; MUID:93326638; PMID:7916639 A; Accession: S34607; MUID:93326638; PMID:7916639
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A;Residues: 1-554 < ALID:
A;Residues: 1-554 < ALID:
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
A;Cross-references: Universase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
C;Keywords: cholinesterase homology < CHE>
F;46-536/Domain: cholinesterase homology < CHE>
F;46-536/Domain: cholinesterase homology < CHE>
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                                  GGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAG
                                                                     TyrSerProThrGluIleThrAlaGlyAspLysArgProValMetValTrpIleHisGly
                                                                                                      TATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGA 456
                                                                                                                                         ThrLeuAsnGluLysMetLysIlePheProIleSerGluAspCysLeuThrLeuAsnIle
                                                                                                                                                                                                               AlaSerIleAsnProProMetCysLeuGlnAspValGluArgMetSerAsnSerArgPhe
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                                                                                                                                                                          CGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCT 1383
                                                                                                                                                                                                                              GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTATCAGTTT 1323
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                 ACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAAAT 1557
                                                 TTCGAAGGAGCCACGGAGGAGGAGTTACTGAGCCGGAAGATGATGAAATACTGGGCT 1497
                                                                                                                                  GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTG----AAGGGGGACATTGTTATG
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carboxylesterase (EC 3.1.1.1) precursor - mouse (;Species: Mus musculus (house mouse) C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 09-Jul-2004 C;Accession: A39060 R;Ovnic, M.; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, Genomics 9, 344-354, 1991 A;Title: Characterization of a murine cDNA encoding a member of the carboxylest A;Reference number: A39060; MUID:91189540; PMID:1840565 A;Accession: A39060 A,Status: preliminary A,Status: preliminary A,Status: preliminary
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A; Residues: 1-554 < OVN>
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                                                                                     GlyLeuValIleGlyGlyArgSerProTyrAsnGlyLeuAlaLeuSerAlaHisGluAsn
                                                                                                                                                                                           GCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAAGGAGGT
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ThrGluLysGluIleLeuProLeuLysIleSerGluAspCysLeuTyrLeuAsnIleTyr
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                                                                                                                                                                         SerProAlaAspLeuThrLysSerSerGlnLeuProValMetValTrpIleHisGlyGly
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Takahashi

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                                     CAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGG 1635
                                                                                            SerArgSerLeuArgAspAlaGlyValSerThrTyrMetTyrGluPheArgTyrArgPro
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A;Molecule type: protein
A;Residues: 19-40 <MAT2>
A;Residues: 19-40 <MAT2>
A;Rote: 28-Lys and 33-Leu were also found
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic seter hydrolase; endoplasmic reticulum; glyc
P;1-18/Domain: signal sequence #status predicted <SIG>
P;19-56/Product: carboxylesterase #status experimental <MAT>
F;19-56/Product: carboxylesterase homology <CHB>
F;51-552/Domain: cholinesterase homology <CHB>
Tightaing site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carboxylesterase (EC 3.1.1.1) precursor - pig
N;Alternate names: proline-beta-naphthylandase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S19307; S23607
C;Accession: S19307; S23607
C;Accession: S19307; S23607
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A;Residues: 1-566 <MAT1>
A;Cross-references: UNIPROT:Q29550; EMBL:X63323; NID:g1930;
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                                                                                                                                                AspLeuPheThrAsnGlyLysGluArgLeuThrLeuGluPhe-----Ser
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                                                                                                                                                                                                                                                  GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC-----TCA
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ProValMetValTrpIleHisGlyGlyGlyGlyLeuValLeuGlyGlyAlaProMetTyrAsp
                                       CCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGAT 492
                                                                                                                                                                                                                    AsnThrThrSerTyrProProMetCysCysGlnAspProValValGluGlnMetThrSer
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                                         GAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGG
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SerValPheGlyPheProLeuLeuLysGlyAsp-----
                                                                                                      TTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGGACATTGTTATGTTCGAAGGAGCCACGGAG
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                        GluGluValSerLeuSerLysThrValMetLysPheTrpAlaAsnPheAlaArgSerGly
                                                                                                                               SerPheSerSerAspLysLysProLysThrValIleGlyAspHisGlyAspGluIlePhe 472
                                                                                                                                                         CAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGC 1395
                                                                                                                                                                                                                                                                CGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACA 1275
                                                                                                                                                                                                                                                                                         GluLeuThrProValAlaThrAspLysTyrLeuGlyGlyThrAspAspProValLysLys 412
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A;Experimental source: liver
(;Superfamily: Cholinesterase; Cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; microsome
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-549/Product: carboxylesterase E1 #status predicted <MAT>
F;50-538/Domain: cholinesterase homology <CHE>
F;79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status
F;221,453/Active site: Ser, His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-023-515-3 (1-1746) x JX0054 (1-549)
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Best Local Similarity:
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    TGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTG
                                                                   TyrLeuAsnIleTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
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                                                                                                                                                                      ThrGlyLysGluSerIleProLeuGluPhe----
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                                                                                                                                                                                                                                                                                                             ValLeuMetSerArgSerLeuArgAspAlaGlyAlaProThrTyrMetTyrGluPheGln
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                                                                                                                                                          GluIlePheSerValPheGlyThrProPheLeuLys------GluGly
                                                                                                                                                                                            GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGACATTGTTATGTTCGAAGGA 1446
                                                                                                                                                                                                                                   TyrArgProSerPheValSerAspGlnArgProGlnThrValGlnGlyAspHisGlyAsp
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ArgAsnGlyAsnProAsnGlyGluGlyLeuProHisTrpProGluTyrAspGlnLysGlu
                                                                              GCCACGGAGGAGGAGGATTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 1506
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A;Note: differences between this sequence and other reports appear R;Kroetz, D.L.; McBride, O.W.; Gonzalez, F.J. Biochemistry 32, 11606-11617, 1993 A;Title: Glycosylation-dependent activity of baculovirus-expressed A;Reference number: A48809; MUID:94032283; PMID:8218228 A;Accession: I61085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'G', 65-185, 'G', 187-361,363-567 < ZSC>
A; Cross-references: GB: X52973; NID: g36421; PIDN: CAA37147.1; PID
R; Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A; Title: Cloning and analysis of a cDNA encoding a human liver
A; Reference number: PS0280; MUID: 92084150; PMID: 1748313
A; Accession: PS0280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA; DNA A;Molecule type: mRNA; DNA A;Residues: 1-3,'PALV', 8-11,'A',13-567 <SHI> A;Residues: 1-3,'PALV', 8-11,'A',13-567 <SHI> A;Cross-references: GB:D21088; NID:g455476; PIDN:BAA04650.1; PID:g458470 A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correspond R;Zschunke, F.; Salmassi, A.; Kreipe, H.; Buck, F.; Parwaresch, M.R.; Radzun, H.J. Blood 78, 506-512, 1991 A;Fitle: cDNA cloning and characterization of human monocyte/macrophage serine esterase-1 A;Reference number: A49816; MUID:91300111; PMID:2070086
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A;Residues: 61-567 <LON>
A;Residues: 61-567 <LON>
A;Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A;Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
Genomics 17, 76-82, 1993
A;Title: Molecular cloning and characterization of a human carboxylesterase
A;Title: Molecular cloning and characterization of a human carboxylesterase
A;Reference number: A47376, MUID:94010913; PMID:8406473
A;Accession: A47376
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A;Residues: 1-567 <MUN>
A;Residues: 1-567 <MUN>
A;Residues: 1-567 <MUN>
A;Cross-references: UNIPROT:P23141; GB:M73499; NID:g179927; PIDN:AAA35649.1; PID:g179928
A;Note: parts of this sequence, including the amino end of the mature protein, were confi
R;Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R.
Life Sci. 48, PL43-PL49, 1991
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A;Cross-references: GB:L07765; NID:g180949; PIDN:AAA35711.1; PID:g180950 A;Accession: A48809 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
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A; Residues: 1-55, 'G', 57-361, 363-535, 'G', 537-567 < KRO1>
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A;Residues: 1-17,'A',18-55,'G',57-535,'G',537-567 <KRO2>
A;Cross-references: GB:L07764; NID:g180947; PIDN:AAA16036.1; PID:g180948
C;GenetLos:
A;Gene: GDB:CES1; HMSE
A;Gene: GDB:CES1; HMSE
A;Gross-references: GDB:128044; OMIM:114835
A;Map position: 16q13-15q22.1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; liver
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-145/Domain: cholinesterase homology <CHE>
F;19-145/Domain: cholinesterase homology <CHE>
F;50-553/Domain: cholinesterase homology <CHE>
F;50-553/Domain: endoplasmic reticulum retention signal #status atypical
F;564-567/Region: endoplasmic reticulum retention signal #status atypical
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carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver N;Alternate names: hydrolase B C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 C;Accession: S62788; SS1203; A55304; S49257 R;Robbi, M.; van Schaftingen, E.; Beaufay, H. Biochem. J. 313, 821-826, 1996
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Arch. Biochem. Biophys. 315, 495-512, 1994

AyTitle: Purification and characterization of two rat liver microsomal A;Reference number: S51202; MUID:95077430; PMID:7986098

A;Molecula Control of two rat liver microsomal A;Reference number: MUID:95077430; PMID:7986098

A;Molecula Control of two rat liver microsomal A;Reference number: MUID:95077430; PMID:7986098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic C; Superfamily: cholinesterase; cholinesterase homology C; Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver F;1-18/Domain: signal sequence #status predicted <SIG>F;1-561/Product: carboxylesterase ES-4 #status experimental <MAT>

F;19-561/Product: carboxylesterase ES-4 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-561 <RO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the sequence in GenBank entry RNU10697, release 107, R;Robbi, M.; Beaufay, H. submitted to the EMBL Data Library, September 1994 A;Reference number: S49257 A;Accession: S49257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-6, 'F', 8-59, 'P', 61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'FY
A; Cross-references: GB: U10697; NID: g562007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Yan, B.; Yang, D.; Brady, M.; Parkinson, A.
J. Biol. Chem. 269, 29688-29696, 1994
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, A;Reference number: A55304; MUID:95050819; PMID:7961958
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Query Match:
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A;Residues: 19-48 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;50-551/Domain: cholinesterase homology <CHE>;221,466/Active site: Ser, His #status predicted;301/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                          TCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACC
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                                        ThrTyrProProMetCysSerGlnAspAlaAlaLysGlyGlnArgMetAsnAspLeuLeu
                                                                               TCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGG---
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                                                              ArgAspAlaGlyAlaProThrTyrMetTyrGluTyrGlnTyrTyrProSerPheSerSer 455
                                                                                                                                             LeuAlaPheIleGlyAspValSerPheSerIleProSerValMetValSerArgAspHis
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ProGlnArgProLysHisValValGlyAspHisAlaAspAspLeuTyrSerValPheGly

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A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-562 COVN-
A;Residues: 1-562 COVN-
A;Cross-references: UNIPROT:Q64176; GB:S80191; NID:g244727; PIDN:AAB21335.1; PID:g244728
A;Cross-references: UNIPROT:Q64176; GB:S80191; NCBIN:80191, NCBIP:80194)
C;Guperfamily: cholinesterase; cholinesterase homology
C;Guperfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum
F;51-552/Domain: cholinesterase homology <CHE>
F;222,467/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carboxylesterase (BC 3.1.1.1) egasyn - mouse
N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein;
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55281
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C;Accession: A55281
R;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;
Genomics 11, 956-967, 1991
A;Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-A;Reference number: A55281; MUID:92147141; PMID:1783403
A;Accession: A55281
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LybAsnAlaThrSerTyrProProMetCysPheGlnAspProValThrGlyGlnIleVal
                                                                                                                                                                           11eSerLeuGluGlyPheThrGlnProValAlaValPheLeuGlyValProPheAlaLys
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TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG
                                                           AsnAspLeuLeuThrAsnArgLysGluLysIleProLeuGlnPheSerGluAspCysLeu
                                                                                        CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTG----
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                                          GGTGCCTTCCTGAAGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTA 1467
                                                                                                   GACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGT
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A; ROJECUAGE : 1-540 < CLON>
A; RESIDURES: 1-540 < CLON>
A; Cross-references: UNIPROT: P10959; GB:M20629; GB:X13587; NID:g203279; A; Cross-references: UNIPROT: P10959; GB:M20629; GB:X13587; NID:g203279; C; Superfamily: cholinesterase; cholinesterase homology C; Keywords: carboxylic ester hydrolase; glycoprotein F; 1-9/Domain: signal sequence #status predicted < SIG>
F; 10-540/Product: carboxylesterase #status predicted < MAT>
F; 41-529/Domain: cholinesterase homology < CHB>
F; 41-529/Domain: cholinesterase homology < CHB>
F; 70, 265, 266, 293, 366, 467/Binding site: carbohydrate (Asn) (covalent) #s
F; 212, 444/Active site: Ser, His #status predicted
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C;Abe: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C;Abccession: A31584
R;Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, P.J.; Pohl, L.R.
Biochem. Biophys. Res. Commun. 156, 866-873, 1988
A;Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for A;Reference number: A31584; MUID:89050119; PMID:2973315
A;Recession: A31584; MUID:89050119; PMID:2973315
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A31584
Carboxylesterase (BC 3.1.1.1) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
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                                TyrLeuAsnIleTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
                                                               TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG
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                                               AlaSerGluGluThrAsnLeuSerLysLeuValMetLysPheTrpAlaAsnPheAla
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Qy 436 GTC	Qy 376 GAC Db 115 Asp	Qy 319 Db 98 Asr	Qy 271 CG/ ::: Db 78 Lys	Qy 211 CCC Db 58 Pro	Qy 151 GTCA: Db 38 Alas	Qy 91 GGC 	Query Match: DB: US-10-023-515-3		F;79,301/Binding F;221,466/Active	F;1-18/Domain: 8 F;19-561/Product F;50-551/Domain: F;558-561/Region	<pre>C; Function: c A; Description: c C; Superfamily: c C; Keywords: carb</pre>	A;Status: not co A;Molecule type: A;Residues: 1-56 A;Experimental s	A; Title: Cloning A; Reference numb A; Accession: S71	R;Yan, B.; Yang, Arch. Biochem. B	C;Species: Rattus no C;Date: 19-Mar-1998	RESULT 13 \$71597 carboxylesterase N;Alternate name	521	Qy 1627 GA	Qy 1567 CA	481
TTGGTGTGGTTCCCAGGAGGT	CTGCCTCTACCTGAACATCTI pCysLeuTyrLeuAsnIleT	CTGCTCTTAGATCAACACATGCTCAAGGTGCA 	CGAGAAGCCACCTCCTACCCTA: ::: ::: Ly6A6nThrThrThrTyrProP:	CCGCTGGGATCCCTGCGAT 	ACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTG :::::: 	CCTTCTGCTGAAGGGCCAC AsnProSerSerProProV	35.63% . 2 (1-1746) x S71597 (1-	2.52e-79 1129.50 Y: 58.64% rity: 43.38%	site: carbohydrate site: Ser, His #sta	gnal sequence #stat carboxylesterase # cholinesterase homo endoplasmic reticu	talyzes conversion olinesterase; choli xylic ester hydrola	mRNA <yan> urce: liver; endopl</yan>	and expression of her: S71597; MUID:951	B.; Yang, D.; Parkinson, A. Slochem. Biophys. 317, 222-234,	#sequence_	prase (EC 3.1.1.1) precursor, names: hydrolase C		GATTTTTGGACCAGCACCATC	;TACCTCCAGCTGGACTTGA ::: /TyrLeuGlnIleGlyAlaT	yAsnGlyAsnProAsnGlyC
GTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGG	CTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCC 	CTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAA 	CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTGAGAGTGG	CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG	GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCC 	GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	Indels: Gaps: 561)	Length: 561 Matches: 236 Conservative: 83 Mismatches: 188	(Asn) (covalent) #st	F;1-18/Domain: signal sequence #status predicted <sig>F;19-561/Product: carboxylesterase #status predicted <mat:f;50-551 <che="" cholinesterase="" domain:="" homology="">F;50-551/Demain: endoplasmic reticulum retention signal</mat:f;50-551></sig>	Function: ;Punction: catalyzes conversion of carboxylic ester to alc; ;Superfamily: cholinesterase; cholinesterase homology ;Keywords: carboxylic ester hydrolase; endoplasmic reticulum;	al translation asmic reticulum	ydrolase C, a member 77656; PMID:7872788	, 1995	Norway rat) revision 17-Apr-1998 #text	sor, liver - rat	527	1647	CAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTG ::: GlyTyrLeuGlnIleGlyAlaThrThrGlnGlnAlaGlnLysLeuLysGlyGluGluVal	${\tt ArgAenGlyAenProAenGlyGluGlyLeuProHisTrpProLysTyrAspGlnLysGlu}$
GCCTCCATCTTTGATGGG 4	CCAAGCTCCCC ::::: erArgMetPro		GlyGlnArgMet		CCTTTGCTGCT roPheAlaLys	.TGGATTCAGGGCAAGCAA 1 		8 6 4	#status predicted	V	o alcohol and		of the rat		:_change 13-Sep-1998					
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1456 GAGGAGAAGTTACTGAGCCGGAAGA 486 GluGluIleLysLeuSerLysMetV	ν σ	1336 CAGTGCTTTGAAGACACGAAGCCGG ::: 452 SerPheSerSerProGlnArgProL	12/6 GCTGATATICACKGAGATUGCTGGTG :::	12	92	72	1051 GAGTGTGGCTTCCTGCTGCCT	991 GATCTATTGTCTCAGAAAGCATTTA 	943 TCTTTCACTCGAC	916 CTGCTGACCCTCAGCCAGAAA 293 LeuLeuGluIleMetGluLysMetA	856 AACAATGCGTCAGACTCTGAGGCCC ::: 273 CysLysThrThrThrSerAlaIlel	796 CTGGAGGCCCATGATTATGAGAAGJ		736	676	1 6	::: ::: 175 TrpGlyPhePheSerThrGlyAsp(556 TTTGGTTTCTTCACCACATGGGATG	496 TCCGCCCTGGCTGCCTATGAGGAC	135 ValMetValTrpIleHisGlyGly
1456 GAGGAGAAGTTACTGAGCCGGAAGATGATGATACTGGGCTACCTTTGCTCGAACCGGG 	ν σ	1336 CAGTGCTTTGAAGACACGAGCCGGCTTTTGTCAAAGCCGACCACCAGCTGATGAAGTTCGC ::: ::: 452 SerPheSerSerProGlnArgProLysAspValValGlyAspHisAlaAspAspValTyr	12/6 GCTCGATATCACAGAGATCCTGGTGCACCTGTCTATGAGTTTCGGCACCGGCCT 1335	12	92		1051 GAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCC		943 TCTTTCACTCGAGTGGTTGATGGTGCTTTCTTTCCTAATGAGCCTCTA 990 ::: :::	916 CTGCTGACCCTCAGCCAGAAA	856 AACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAG :::	796 CTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGT	:::::: :::	736)	1 6	175 TrpGlyPhePheSerThrGlyAspGluHisSerArgGlyAsnTrpGlyHisLeuAspGln	556 TTTGGTTTCTTCACCACATGGTATCAGCATGCTTCCGGGGAGGAGGGTT	496 TCCGCCCTGGCTATGAGGACGTGCTGCTGTGTGGTCCTGCCAGTACCGGCTAGGAATA	135 ValMetValTrpIleHiBGlyGlyGlyLeuThrGlnGlyGlyAlaSerThrTyrABpGly 154

Qy 277 GCCACCTCCTACCCTAATTTGTGCCTCCAGAAC 309	Qy 217 CTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAA 276	Qy 157 GTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTGCTCCCCCG 216	Qy 97 TCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGATTCAGGGCAAGCAA	2 CysLeuTyrAlaLeuIleLeuValPheLeuAlaAlaPheThrAlaGlyGlyHis 19	37 TGCTTTTTCCTGATTCTCCA	h: 35.43% Indels: 2 Gaps: 515_3 (1_1746) x JC2447 (1_561)	. NO.: 8.04e-79 1123.00 1123.00 1123.07 1123.07 1123.07	F;79,107,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;721,466/Active site: Ser, His #status predicted	C;Keywords: Carboxylic ester hydrolase; glycoprotein F;1-18/Domain: signal sequence #status predicted <sig> F;19-561/Product: Carboxylestersee ES-3 #status predicted <mat> F:60-551/Domain: cholinestersee homology <che></che></mat></sig>	A; Molecule type: mRNA; A; Molecule type: mRNA; A; Residues: 503-554, 'R', 556-561 <med> A; Residues: 503-554, 'R', 556-561; MED> A; Cross-references: EMBL: X56295; NID: g57557; PIDN: CAA46390.1; PID: g57558 C: Superfamily: Cholinesterase; Cholinesterase homology</med>	esterase family ex 23460; MUID:922990	A;Cross-references: UNIPROT:Q63108; GB:X81395; NID:g550146; PIDN:CAA57158.1; PID:g550147 A;Experimental source: liver R;Medda, S.; Proia, R.L. Fur J. Biochem 206 801-806 1992	2447; MUID:95032008; PMID:7945287	xvleaterage Ra	C.Date: 29-Mar-1995 #semience revision 26-May-1995 #text change 09-Jul-2004	546 ThrGlnLeuLeu	:::	Db	стваства
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1264 GCACTGATCACAGGTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT 1323 	ProAspArgAsnLysAspGlnLeuLeuGluLeuIleGlyAspValIlePheGlyValPro	::::: ::: ::: ::: ::: ::: ::: ::: ::	:::	CTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTG	1036 GGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATC 1092 :::	976 CCTAATGAGCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC	952 975 	901 AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACT 951 :: :: 288 LysThrGluGluLeuLeuGluThrThrLeuLysLeuAsnLeuPheSerLeuAspLeu 307	841 GCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACA 900 	784 ATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGAGCTGCAGGTGGTT 840	724 ATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCC 783 ::: :::	664 GACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTT 723	604 TTCAAGGACCAGGTGGCTGTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGG 663 	544 CGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCC 603 171 ArgLeuGlyIleTrpGlyPhePheSerThrGlyAspGluHisSerArgGlyAsnTrpGly 190	484 ATCTTTGATGGGTCCGCCCTGGCTGTATGAGGACGTGCTGGTTGTGGTCGTCCAGTAC 543 	424 TCCAAGCTCCCCGTCTTGGTGTGTGTTCCCAGGAGTGCCTTCAAGACTGGCTCAGCCTCC 483 ::: ::: 131 AspArgLeuProValMetValTrpIleHisGlyGlyGlyLeuValLeuGlyGlyAlaSer 150	364 GGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCCACGCCGATACAGGC 423	310TCAGAGTGGCTGGTCTTAGATCACATGCTCAAGGTGCATTACCCGAAATTC 363 ::: 100 LeuLeuThrAsnTrpGluGluAsnIleSerLeuGlnPhe 112	ThrThrSerTyrProProMetCysSerGlnAspProValAlaGlyGlnIleValAsnAsp

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A;Mclecule type: mRNA
A;Residues: 1-264, 'K', 266-565 < ROB2>
A;Cross-references: EMBL:X51974; NID:g56898; PIDN:CAA36236.1; PID:g56899
A;Cross-references: EMBL:X51974; NID:g56898; PIDN:CAA36236.1; PID:g56899
R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Blochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal carbox
A;Reference number: S51202; MUID:95077430; PMID:7986098
A;Accession: S51202
A;Molecule type: protein
A;Residues: 19-48 < MOR>
R;Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal sequence diversity r
A;Accession: S23460; MUID:92299008; PMID:1606962
A;Accession: S23460; MUID:92299008; PMID:1606962
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-185,'Q',187-422,'M',424-505,'N',507-565 < MED>
A;Cross-references: EMBL:X55296; NID:957553; PIDN:CAA46391.1; PID:957554
A;Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Biochem. J. 274, 693-697, 1991
A;Molecule type: protein
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-00;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-00;A;C;Accession: S10367; S12466; S51202; S23460; S14361
R;Robbi, M.; Beaufay, H.; Octave, J.N.
Biochem. J. 269, 451-458, 1990
A;Title: Nuclectide sequence of cDNA coding for rat liver pI 6.1 eslochem. J. 269, 451-458, 1990
A;Title: Nuclectide sequence of cDNA coding for rat liver pI 6.1 eslochem. J. 269, 451-458, 1990
A;Reference number: S10367; MUID:90351366; PMID:2386485
A;Recession: S10367
A;Accession: S10367
A;Molecule type: mRNA
A;Residues: 1-565 <ROB1>
A;Cross-references: UNIPROT:Q9R135; EMBL:X51974
A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. R;Robbi, M.
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A;Accession: S12468
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C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-565/Product: carboxylesterase #status predicted <WAT> F;50-551/Domain: cholinesterase homology <CHE> F;79,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221,466/Active site: Ser, His #status predicted
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TrpSerGlu-------LeuArgAlaLysGluAlaAlaGluGluPro 557
                                                                                                                                  CTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTT 1632
                                                                                                                                                                               GlySerProAsnGlyGlyGlyLeuProHisTrpProGluTyrAspGlnLysGluGlyTyr 524
                                                                                         LeuLysIleGlyAlaSerThrGlnAlaAlaGlnArgLeuLysAspLysGluValAlaPhe
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Search completed: June 15, 2005, 08:55:41 Job time : 60.53 secs

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-Q=(cgn2 1)(USPYO spool)664091/runat 14062005 -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
-WIITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALICN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6664091 @CGN 1 1 389 @runat 14062005 133459 9335 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

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MEDLINE-2238257; PubMed-12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Borak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S. J. Marra M.A.
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05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLJ31547 protein.
Name=FLJ31547;
  SEQUENCE FROM N.A.
TISSUE=PCR rescued clones;
                                                                   Proc.
                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse CDNA sequences.";
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TISSUE=PCR rescued clones;
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--- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; BC065501; AAH69501.1; --
HSSP; P12337; IX4Y.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR003018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00142; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00141; CARBOXYLESTERASE B 1; 1.
Hydrolase.
SEQUENCE 575 AA; 63926 MW; 6F5B735BDEFC9C09 CRC64;
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             GGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTAT
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                                                                                  CTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATG
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                     PRELIMINARY;
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RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Oteuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Makamatsu A., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Minomiya K., Ishibashi T., Yamashita H., Kondo H., Sugawara M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Aloe K., Kamihara K., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Minomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Aloe K., Kamihara K., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Actsuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,
RA Ono T., Yamada K., Puji Y., Ozaki K., Hirao M., Ohnori Y.,
RA Ono T., Yamada K., Puji Y., Ozaki K., Hirao M., Ohnori Y.,
RA Matani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matani K., Vada T., Nakamura Y., Ohara O., Isogai T., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Matai K., Vada T., Nakamura Y., Ohara O., Isogai T., Namashita R.,
RA Matai K., Vada T., Nakamura Y., Ohara O., Isogai T., Namashita R.,
RA Matai K., Vada T., Nakamura Y., Ohara O., Isogai T., Namashita R.,
RA Matai 
                                                                                                                                                                                                                                                                                                        ARBELINE=22388257; Pubmed=1,477932; DOI=10.1073/pnas.242603899;

AS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

AK Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AA Bischer M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AB Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AR Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AR Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

AR Abas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

AR Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

AN Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

AN Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

AN Hilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

AN Milting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

AN Arres S. T. Max A., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                  TISSUE-PCR rescued clones;
Strausberg R.;
                                                                                                                                                                                                                                   Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PCR rescued clones;
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SIMILARITY: Belongs to the type-B
L; AK056109; BAB71094.1; -.
L; BC069548; AAH69548.1; -.
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                                                                          (APR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36:40-45(2004).
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; Coesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Hydrolase; Hypochetical protein.
Lydrolase; Hypochetical protein.
SEQUENCE 525 AA; 58200 MW; 7724878B8A22F215
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RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
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RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
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RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
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RA Aloniya K., Katsuta N., Sato S., Yosida M., Hotuta T., Kusano J.,
RA Cono Y., Takahashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Actsuka S.,
RA Moriya S., Komai F., Hara R., Takami S., Terashima Y., Suzuki O.,
RA Matsumawa H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Marayawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shizai Y., Takahashi Y., Namashita R.,
RA Nishasi Y., Vada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
CDNAS, "., Makagawa T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyazaki M., Yamashita T., Taira H., Suzuki A.;

I "cauxin family protein.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

C -- SIMILARITY: Belongs to the type-B carboxylesterase/lips

R EMBL; ABL86392; BAJ35015.1; -.

R GO; GO:0003824; F:catalytic activity; IEA.

R InterPro; IPR002018; CarbesteraseB.

R InterPro; IPR000379; Ser_estrs.

R Pfam; PF00135; COesterase; 1.

R PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

R PROSITE; PS00121; CARBOXYLESTERASE B 2; 1.
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Q6AW47;
Q5-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
MCBI_TaxID=9615;
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"cauxin family protein.";

submitted (AUG-2004) to the EMBL/GenBank/DDBJ dat
-i-SIMILARITY: Belongs to the type-B carboxylest
EMBL; AB186393; BAD35016.1; -.

GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR002079; Ser_estrs.

Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

Hydrolase.

SEQUENCE 575 AA; 64166 MW; 3EB9D85981D9DE0A C
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Mammalia; Eutheria; Rodentia;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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                  ThrLysGluTyrPheHisGlyLysHisSerProThrAspIleArgAspThrLeuLeuAsp
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                              Miyazaki M., Kamiie K., Soeta S., Taira H., Yamashita T.;

"Molecular cloning and characterization of a novel carboxylesterase-
like protein that is physiologically present at high concentrations i
the urine of domestic cats (Felis Catus).";

Biochem. J. 370:101-110(2003).

-i- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

EMBL; AB045377; BAC22577.1; -.

EMBL; AB045377; BAC22577.1; -.

EMBL; AB04577; Fihydrolase activity; IEA.
                                                                                                                                                                                                            PROSITE; PS00122;
PROSITE; PS00941;
Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=22458314; PubMed=12401131; DOI=10.1042/BJ20021446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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Q8I034;
Q8I034;
Q8I034 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein.
                                                                                                                                                                No.:
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ArgSerLeuAlaLeuTyrLeuValHisThrPheLeuAsnIleProThrGlnTyrLeuHis
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C TISSUE-Temporal lobe right;
C TISSUE-Temporal Nobe right;
A OSAda N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.
Suzuki Y., Sugano S., Hashimoto K.;
Submitted (APR-2001) to the EMBL/JeenBank/DDBJ databases.
C -!- SIMILARITY: Belongs to the type-B carboxylesterase/lip;
R EMBL; AB060873; BAB46884.1; --
R HSSP; P12337; 1K4Y.
R InterPro; IPR002018; CarbesteraseB.
R Pfam; PF00135; COesterase; 1.
W Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95KH3 PRELIMINARY; PRT; 361 AA.
Q95KH3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
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ATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCA
                                                                                        serValSerValGlyGlnLysLeuLysGluGlnGluValGluPheTrpMetAsnThrIle
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52.89%
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Matches:
Conservative:
Mismatches:
Indels:
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
                                                                                    Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Anseriformes; Anatida
                                                                                                                                                            Fatty acyl-CoA hydrolase precursor, (Thioesterase B).
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SEQUENCE FROM N.A., AND TISSUB=Uropygial gland;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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"Molecular cloning and sequencing of thioesterase B gene associated wit stimulation of expression of the thioesterase B gene associated wit hormonal induction of peroxisome proliferation.";

J. Biol. Chem. 268:14278-14284(1993).

-I-FUNCTION: Fatty acid biosynthesis chain termination and release the free fatty acid product is achieved by hydrolysis of the the ester by a thioesterase. This thioesterase may be associated wit peroxisome proliferation and may play a role in the production peroxisome proliferation and may play a role in the production.

-I-TISSUE SPECIFICITY: Highest levels in uropygial gland, much low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

Direct protein sequencing; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A47162; A47162.
HSSP; O77540; 1K4Y.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L05493; AAA49223.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in liver and kidney.
SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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                                                   GlyGlnTyrLeuSerAspAlaIleThrAsnArgLysGluLysValArgLeuGlnIleSer
                                                                                     GATCAACACATGCTC
                                                                                                                    ---ValargaspalaalaSerTyrProProMetCysLeuGlnAspLys--
                                                                                                                                      TTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTA
                                                                                                                                                                                    LysProProValGlyProLeuArgPheSerGluProGlnProGluProTrpLysGly
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Acyl-ester intermediate (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
N-linked (GlcNAc. . .) (Potential).
103E35D90A037F6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                (1-557)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                     AAGGTGCATTACCCGAAATTCGGAGTGTCA
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                                                                          VallysAlaAspHisAlaAspGluIleAlaPheValPheGlyLysProPheLeuAlaGly
                                                                                                                 GTCAAAGCCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGG
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RC STRAIN=FYB/N; TISSUE-Colon, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,

RA Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Randin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan J., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Tand monies G.J., Marra M.A.;
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(991WG0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 28, Last sequence update)
05-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase 2 (Carboxylesterase ML3 precursor).
Name=Ces2; Synonyms=ces2A3;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalli; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                        Strausberg
Submitted
Strausberg
                                                                            Submitted (JUN-2002)
                                                                                                              SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                          Strausberg
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                    STRAIN=FVB/N; TISSUE=Colon,
                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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GO; GO:005615; C:extracellular space; Tefam; PF00115; Coesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_1; PROSITE; PS00121; CARBOXYLESTERASE B_2;
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                                                              GACCACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGTGCCTTC-----CTGAAGGGGGAC
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                                                        STRAIN=C57BL/6J; TISSUB=Ovary and uterus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itch M., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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STRAIN-C57BL/6J; TISSUE-Cvary and uterus;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
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QBBK48;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, clone:5031415B19 product:similar
to CARBOXYLESTERASE (EC 31.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (CCCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
(9030624L02Rik protein).
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Ovary and uterus; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Brownstein M.J., Walin R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Korsywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Korsywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Submitted (OUL-2003) to the EMBL
-!- SIMILARITY: Belongs to the CEMBL; AK077248; BAC36707.1; -.
EMBL; BC055062; AAH55062.1; -.
HSSP; P12337; 1K4Y.
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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30; GO:0005615; C:extracellular space;
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
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01-JAN-1998 (TYEMBLYEL. 05, Last sequence update)
01-MAR-2004 (TYEMBLYEL. 26, Last annotation updat
Carboxylesterase precursor (EC 3.1.1.1).
Mesocricetus auratus (Golden hamster).
                                                                                GO; GO:0004091; F:carboxylesterase activity; GO; GO:0016787; F:hydrolase activity; IEA. InterPro; IPR002018; CarbesteraseB. InterPro; IPR000886; ER_target_S. InterPro; IPR000379; Ser_estrs_PR051TE; PS00122; CARBOXYLESTERASE_B_1; 1. PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1. PROSITE; PS00941; ER_TARGET; UNKNOWN_1.
                                                                                                                                                                        STRAIN-Syrian golden;
Sone T., Wang C.Y.;
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                           SEQUENCE
                                                                                                                                                                                                                                                               "Microsomal amidases and carboxylesterases.";
(In) Guengerich F.P. (eds.);
COMPREHENSIUE TOXICOLOGY VOLUME 3, Biotransformation, pp.265-281,
Pergamon, Oxford (1997).
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Q8BM97;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male colon cDNA, RIKEN full-length enriched
library, clone:9030624102 product:similar to CARBOXYLESTERASE (EC
3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE).
                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=C57BL/60; TISSUE=Colon;

MEDLINE=99279253; PubMed=10349636;

Carninci P. Hayashizaki Y.;

"High-efficiency full-length cDNA of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the col
  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                     Name=9030624L02Rik;
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Rodentia;
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                                                                                                                                                                                             cloning
                                                                                     DOI=10.1038/35055500
                                                                                                                                                                                                                                    DOI=10.1016/S0076-6879(99)03004-9;
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RA Hyushida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Koyawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Kurihara C., Matsuyama T., Miyazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Sulmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
C. -- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
RMBL; AKO33563; BAC28361.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Colon;
MEDILINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDILINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Colon; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                             InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PP00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.", Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                            HSSP; P12337; 1K4Y.
MGD; MGI:2443170; 9030624L02Rik.
GO; GO:0005615; C:extracellular space;
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AspGluTyrGlyTrpIleLeuProThrIleMetAspProAlaGlnLysIleGluGluIle
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                                             LeuProProGluCysGlyAspLeuLeuMetGluGluTyrMet
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RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., MAX S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonahlo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulahy S.W.,
RA Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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Name=BC015286;
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                         Strausberg R.;
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STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
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Belongs to t
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  e EMBL/GenBank/DDBJ databases.
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InterPro; IPR000379; Ser_estrs.
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PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
Hydcrolase; Hypothetical protein.
SEQUENCE 556 AA; 61927 MW; 58DE05A3;
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|GlyValAlaLeuLeuProTyrLeuIleThrAspThrSerGluMetValSer-----Thr
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XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

XX Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

XX Altschall S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschall S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Lington M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,

XX Stapleton M., Soares M.B., Bonaldo M.F., Casninci P., Prange C.,

XX Altschards N., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., MocWellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., MocWellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

XX Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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XX Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

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XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

XX Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Gerhard D.S.;

Klein S., Gerhard D.S.;

Klein S., Gerhard D.S.;

Klein S., Gerhard D.S.;

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

-:- SIMILARITY: Belongs to the type-B carboxylesterase/lipase in the type-B carboxylesterase/lipase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxylesterase in the type-B carboxy
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MEDLINE=22341132;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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::::::||||||||||||:::|||
LeuSerLyeGlyLeuPheHisArgAlaIleSerGluSerGlyValAlaIleLeuProGly 265
GTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCT 1305
                                                                      AlaLeuPro---PheValHisSerPheThrSerValValProPheIleMetGluGluTyr
                                                                                                                                                ATCCCGCCTCAGTATTTGCAC------CTTGTGGCTAATGAATAC
                                                                                                                                                                                   -----IleSerGlyTyrArgGluGlyMetGluLysLysAspileGlnSerIleLeuVal
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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                          Sone T., Kunitomo T., Isobe M.;

Submitted (JAN-1998) to the EWBL/GenBank/DDBJ databases.

- I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EWBL; ABD10632; BAA25691.1; -.

HSSP; P37967; 1QE3.

GO; GO:0014091; F:carboxylesterase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002018; Ser_estrs.
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                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                     Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
                                                                                                                             No.:
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Wistar; TISSUE=Small intestine, Sone T., Kunitomo T., Isobe M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                         Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=carboxylesterase;
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     ATGCCACAGGGA----CTTACTTCATCTGCTTCACAATGGTGCTTTTTTCCTGATTCTCCAG
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ProProGluProProGluProTrpSerGlyValArgAspAlaThrSerGlnProAlaMet
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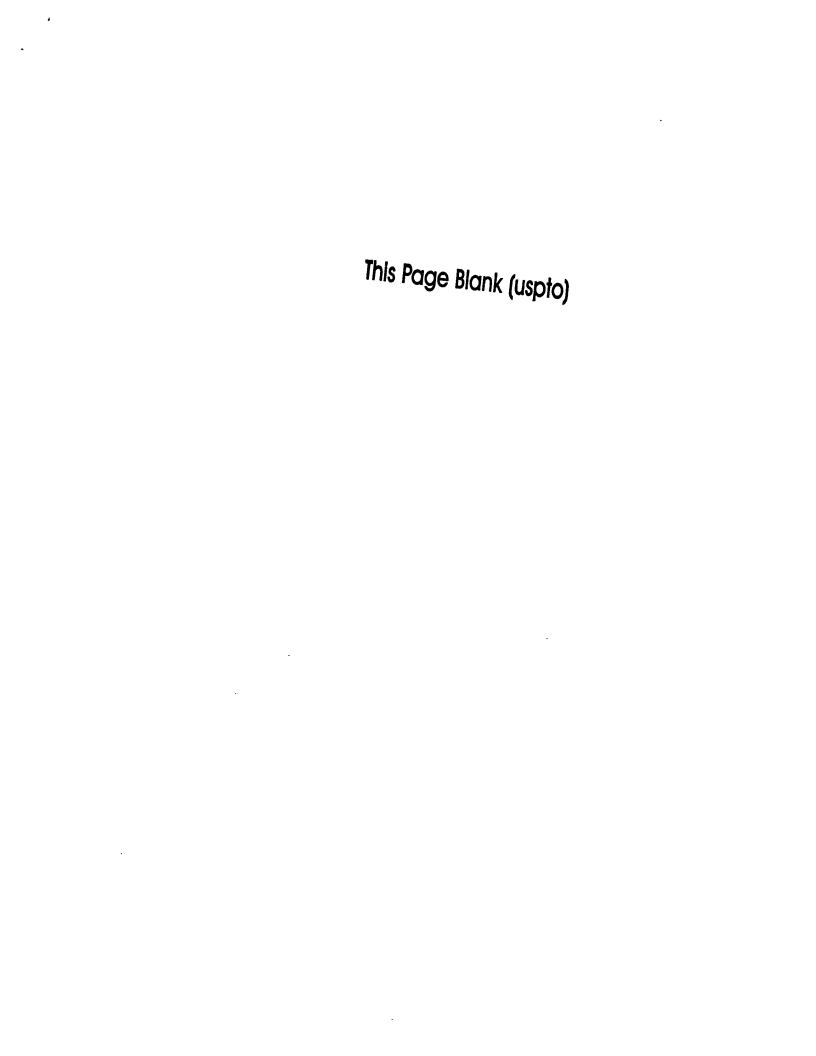
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                                                       ProAsnSerGluGlyLeuProTyrTrpProAlaLeuAspHisAspGluGlnTyrLeuGln
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Search completed: June 15, 2005, 08:53:13
Job time : 183.861 secs



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Result
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Listing first 45 summaries
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-MODEL-frame+ n2p.model -DEV=xlh
-Q-/cgn2 1/USPTO spool/6664091/runat 14062005 133500 9360/app query.fasta 1.4238
-DB-Issued Patents AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-WODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=664091 @CGN_1 54 @runat_14062005_133500_9360 -NCPU=6 -ICPU=3 -NO_MMAP
-LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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US-09-595-682B-28

US-09-949-016-6426

US-09-949-016-9670

US-09-595-682B-21

US-09-595-682B-21

US-09-595-682B-26

US-09-564-737-2

US-09-140-933-2

US-09-146-651-2

US-09-146-651-2

US-09-160-515-2

US-09-264-737-1
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Sequence 28, Appl
Sequence 6426, App
Sequence 9670, Ap
Sequence 21, Appli
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equence 6, App	equence 6,	equence 1,	equence 4, Appl	equence	equence 22,	equence 23, App	equence 20, Ap	equence 70	nce 7063,	equence 2,	equence 2,	equence 21	equence 19	equence 2,	equence 2,	equence 25	equence 21	equence 22	equence 2,	equence 23	equence 1,	equence 20,	equence 838	equence 688	equence 838	equence 4,	equence 29,	eguence 27,	equence 31,	equence 30,	equence 28,	Sequence 26, Appl

ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-023-515-2
US-10-023-515-3 (1-1746) x US-10-023-515-2 (1-581)
                                                    Query Match:
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Patent No. 6664091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                   SEQ ID NO 2
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
EILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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Conservative:
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                                                    APPLICANT: Danks, Mary K.

APPLICANT: Potter, Philip M.

APPLICANT: Houghton, Peter J.

TITLE OF INVENTION: Compositions and Method
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
         Alignment Scores:
Pred. No.:
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                                             Score:
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                                                          Pred. No.:
                                                                      Alignment Scores:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PRILING DATE: 2000-09-08
PRIOR PRILING DATE: 2000-09-08
PRIOR PRILING DATE: 2000-09-08
                                                                                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 6426
LENGTH: 559
TYPE: PRT
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                                                                                                               ORGANISM: Human
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                                AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT 969
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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| SerMetLeuAlaAlaLeuGluAsnValValValValIteIleGlnTyrArgLeuGlyVal 199
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                                                                                                              AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT
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 AspThrGlnLysGluMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr 395
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| IleValGlyValAsnAsnAsnGluPheGlyTrpLeuIleProLysValMetArgIleTyr 375
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Percent Similarity:
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Query Match:
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APPLICANT: Potter, Philip M.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
TITLE REFERENCE: SJ-005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR PILING DATE: 1998-02-19
PRIOR PILING DATE: 1998-02-19
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SCOTWARE: Patentin Ver. 2.0
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                                                      US-10-023-515-3 (1-1746) x US-09-595-682B-21 (1-565)
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                   LENGTH: 565
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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                                                                                  GlyAspProLysGluAsnThrAlaPheLeuThrThrValIleAspGlyValLeuLeuPro
                                                                                                                                                                  ThrGluGluGluLeuMetGluValThrLeuLysMetLysPheMetAlaLeuAspLeuVal 308
                                                                                                                                                                                            CCCTCCAAGGAGCTGCTG-----ACCCTCAGCCAGAAA------
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|LeuProValMetValTrpIleHisGlyGlyGlyLeuMetValGlyGlyAlaSerThrTyr 152
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US-10-023-515-3 (1-1746) x US-09-264-737-2 (1-566)
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                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09264737A Patent No. 6107549
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21 (10551) RLB3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                      LENGTH: 566
TYPE: PRT
ORGANISM: Rabbit
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                       APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
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                                                Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                            TYPE: PRT ORGANISM: Oryctolagus cuniculus
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                   CCCTCCAAGGAGCTGCTG-----ACCCTCAGCCAGAAA------
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                                                                                                                                   SerSerLeu------PheArgLysAsnThrLysSerLeuAlaGluLysIleAla
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US-08-845-295A-2
; Sequence 2, Application
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                                                ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE. Microsoft word
CURRENT APPLICATION DATA:
                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                      STATE: T
                                                                                                             CITY:
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                                                                                                  Tennessee
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                                                                                      USA
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
APPLICATION NUMBER: US/08/845,295A FILING DATE: 25-April-97
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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APPLICATION NUMBER: US 60/017
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
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ValLysAsnThrThrSerTyrProProMetCysCysGlnAspProValValGlnMet
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        AACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTC
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                    TyrAspGlnGluGluGlyTyrLeuGlnIleGlyValAsnThrGlnAlaAlaLysArgLeu
                                          TATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTC
                                                                                                                          TTCGAAGGAGCCACGGAGGAGAAGATTACTGAGCCGGAAGATGATGAAATACTGGGCT 1497
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APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzyma:
TITLE OF INVENTION: 2-Keto
NUMBER OF SEQUENCES: 3
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APPLICATION NUMBER: US/09/140,933
FILLING DATE: 27-August-98
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILLING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
NAME: Cheryl J. Tubach
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Patent No. 602271
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70-
TELECOMMUNICATION INFORMATION: 423-229-6.89
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TYPE: Amino Acid
TOPOLOGY: Linear
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STATE: Tennesse
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                                                                                                                                                                    SerLeuGluGlyLeuAlaPheThrGlnProvalAlaValPheI
                                                                                                                                     GlnProAlaSerProProValValAspThrAlaGlnGlyArgValLeuGlyLysTyrVal
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US-09-146-661-2
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                                            TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enzymatic Process for the Manufacture of TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gulonic Dylamore, acid NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
ETLING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft word
CURRENT APPLICATION DATA:
                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
TOPOLOGY: Li
                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/14 FILING DATE: 03-Septmeber-98
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CITY: Kingsport
                                TYPE:
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                                GlnIleAlaValLeuAlaGlyCysLysThrThrThrSerAlaValPheThrPheValHis
                                                                                            GluSerGlyValAlaLeuThrValAlaLeuValArgLysAspMetLysAlaAlaAlaLys
                                                                                                                                                              SerValSerValLeuValLeuSerProLeuAlaLysAsnLeuPheHisArgAlaIleSer 254
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AsnTrpGlyHisLeuAspGlnValAlaAlaLeuHisTrpValGlnGluAsnIleAlaAsn
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US-09-150-515-2
                                                 Sequence 2, Application US/09150515
Fatent No. 6271006
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company STREET: P.O. Box 511 CITY: Kingsport
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch d
COMPUTER: IBM Compatibl
OPERATING SYSTEM: Windo
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APPLICATION NUMBER: US 60/017,879;

FILING DATE: 17-MBy-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05
FILING DATE: 09-SEP-1998
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   TCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGAC----
                                    ArgGlyArgLeuProValMetValTrpIleHisGlyGlyGlyLeuValLeuGlyGlyAla 154
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                                         GlnTyrArgProSerPheSerSerAspLysPheThrLysProLysThrValIleGlyAsp
                                                                                                                             CGGCACCGGCCTCAGTGCTTTGAAGAC-----ACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                                                                                                                                                                                       GluLeuThrProValAlaThr-----PheThrAspLysTyrLeuGlyGlyThrAspAsp
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                                                                                                                                                                                                                                                                                                                             LysSer------ProGlu 404
                                                                                                                                                                                                                                                                                                                                                        GGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAG 1158
                                                                                                                                                                                                                                                                                                                                                                                    MetGlyPheProLeuSerGluGlyLysLeuAspGlnLysThrAlaThrSerLeuLeuTrp
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                                                                     CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
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APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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ORGANISM: Rabbit
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                                                       CACATGCTC-----
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                                                                                                            HisMetLeuSerGluLeuPheThrAsnArgLysGluAsnIleProLeuLysPhe----
                                                                                                                                                                   AsnThrThrSerTyrProProMetCysSerSerAspAla------ValSerGly 76
                                                                                                                                                                                                                           ProLeuGlySerLeuArgPheAlaProProGlnProAlaGluSerTrpSerHisValLys
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ThrGluGluLeuMetGluValThrLeuLysMetLysPheMetAlaLeuAspLeuVal 282
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                      CTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTGAGCCGG 1476
                                                                                                           CCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTC 1416
                                                                                                                                             GlyAlaProThrTyrMetTyrGluTyrArgTyrArgFroSerPheSerSerAapMetArg
                                                                                                                                                                                 GGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAG 1356
                                                                                                                                                                                                                    LeuAlaAspLeuLeuPheGlyValProSerValAsnValAlaArgHisHisArgAspAla
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                                                                                                                                                                                                                                                                                              GluLysTyrLeuGlyGlyThrAspAspProValLysLysLysAspLeuPheLeuAspMet 393
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-GluGlyAlaThrGluGluGluIleLysLeuSerLys 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 425-276
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                           MOLECULE TYPE: PHYPOTHETICAL: YES ANTI-SENSE: YES FRAGMENT TYPE: NO ORIGINAL SOURCE: ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: br
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEPHAX: (703) 425-2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Okeana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.25
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ZIP: 22031
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508 AlaAlaGinLysLeuLysAspLysGluValAlaPheTrpThr
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                                                                                 GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGA 1446
                                                                                                                          TyrArgProSerPheSerSerAspMetLysProLysThrValIleGlyAspHisGlyAsp 357
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US-10-023-515-3 (1-1746) x US-08-446-100-28 (1-454)
                                          Query Match:
                                                        Best Local Similarity:
                                                                                      Score:
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                                                                                                                                              US-08-446-100-28
                                                                                                   Pred. No.:
                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/446
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION UNMBER: 32,535
REFERENCE/DOCKET NUMBER: broc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed M
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 425-27
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acid
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: YES
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                                                            TyrArgProSerPheSerSerAspMetLysProLysThrValIleGlyAspHisGlyAsp
                                                                                                                                           ValileValAlaArgAsnHisArgAspAlaGlyAlaProThrTyrMetTyrGluPheGln
                                                                                                                                                                   CTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGG 1326
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                                                                                                                                                                                                                                                                    ACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTTGTGGTCCCTGCA 1266
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HYPOTHETICAL: YE
ANTI-SENSE: YES
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100 FILING DATE: 19-MAY-1995 CLASSIFICATION: 435
ATTORNEY / ACTEM
                                                                                                                          . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
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NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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STATE: VA
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|GluThrGlnArgHisSerThrLeuLeuGlyThrValIleAspGlyMetLeuLeuLeuLys 217
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432 AlaPheTrpThrAsn 436
                                          CAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTG 1626
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Search completed: June 15, 2005, 08:57:41 Job time : 53.3868 secs



Result

Query

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Database :
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-Q=/cgn2 1/USPTO_spool/664091/runat 14062005 133501 9433/app query.fasta 1.4238
-DB=-Dublished_Applications_AA -QFMT=Fastan -SUFFIX=n2p, rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pot -THR_MXX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=6664091 @CGN 1 1 295 @runat 14062005 133501 9433
-NCPU=6 -ICPU=3 -NO_MAAP -LARGEQUERY -NGEG_SCORES=0 -WAIT -USPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	1	10	9	8	7	6	v	4	ω	N	بر	No.
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ALIGNMENTS

US-10-023-515-2

| Sequence 2, Application US/10023515
| Sequence 2, Application US/20020182636A1
| GENERAL INFORMATION:
| APPLICANT: Curtis, Rory A. J.
| APPLICANT: Curtis, Rory A. J.
| TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
| TITLE OF INVENTION: 53010, WEYSER AND USES THEREOF
| FILE REFERENCE: 10448-122001
| CURRENT APPLICATION NUMBER: US/10/023,515
| CURRENT APPLICATION NUMBER: 60/256,369
| PRIOR APPLICATION NUMBER: 60/256,369
| PRIOR APPLICATION NUMBER: 60/279,508
| PRIOR APPLICATION NUMBER: 60/279,508
| PRIOR APPLICATION NUMBER: 60/279,508
| PRIOR PILING DATE: 2001-03-28
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LENGTH: 581

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo
US-10-023-515-2
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Sequence 2, Application US/10674636

Sequence 2, Application US/10674636

Publication No. US20040086922A1

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/674,636

CURRENT FILING DATE: 2003-09-29
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                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
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Sequence 46, Application US/10757262
Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: KATICHEL, Venkateswarlu
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: NUCENTION: US-5053
TITLE OF INVENTION: 10547, 115, 579, 15985,
TITLE OF INVENTION: 2158, 8263, 15402, 1620
TITLE OF INVENTION: 2543, 9626, 13231, 3240
TITLE OF INVENTION: 2543, 9626, 13231, 3240
TITLE OF INVENTION: 55053
FILE REFERENCE: MPT03-007PIRNOMNIM
CURRENT APPLICATION NUMBER: US-60/444, 783
FILING DATE: 2003-01-15
FRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US-60/444, 783
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US-60/449, 75
PRIOR APPLICATION NUMBER: US-60/449, 75
PRIOR APPLICATION NUMBER: US-60/449, 74
PRIOR FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US-60/478, 74
PRIOR APPLICATION NUMBER: US-60/478, 74
PRIOR APPLICATION NUMBER: US-60/478, 74
PRIOR APPLICATION NUMBER: US-60/478, 74
PRIOR FILING DATE: 2003-05-19
PRIOR PRILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US-60/49, 594
PRIOR APPLICATION NUMBER: US-60/49, 594
PRIOR APPLICATION NUMBER: US-60/49, 594
PRIOR APPLICATION NUMBER: US-60/49, 594
PRIOR APPLICATION NUMBER: US-60/49, 594
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PRIOR APPLICATION NUMBER: US-60/49, 594
PRIOR APPLICATION NUMBER: US-60/49, 594
PRIOR FILING DATE: 2003-09-26
PRIOR PILING DATE: 2003-09-26
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; TYPE: PRT
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Best Local Similarity:
Query Match:
DB:
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UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
13751, 52872, 1463, 20739, 32544, 43239, 44373, 51164,
53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
18547, 185, 14303, 16816, 17827, 32620, 577, 619, 1423,
32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
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                                                   CCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAG 1320
                                                                                                     SerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValVal
                                                                                                                       AlaProGluIleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsnIle
                                                                                                                                                                                                                                                           GCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATC 1140
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                                ProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGlu
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CURRENT FILING LATE: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/USO1/49232

PRIOR PILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR PILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-12-20

PRIOR PILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-01-09

PRIOR PRIOR APPLICATION NUMBER: 60/260,482

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/264,922

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR APPLICATION NUMBER: 60/266,997

PRIOR APPLICATION NUMBER: 60/266,997

PRIOR APPLICATION NUMBER: 60/26,988

PRIOR APPLICATION NUMBER: 60/276,988

PRIOR APPLICATION NUMBER: 60/276,988

PRIOR PILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/281,535

PRIOR APPLICATION NUMBER: 60/289,622

PRIOR PILING DATE: 2001-04-04

PRIOR PILING DATE: 2001-04-04

PRIOR PILING DATE: 2001-05-28

NUMBER OF SEG ID NOS: 110

SOPTWARE: FASTSEQ for Windows Version 4.0

SEG ID NO 91

LENGTH: 575
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US-10-451-168-91
S-91
Sequence 91, Application US/10451168
; Publication No. US20040091969A1
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          Alignment Scores: Pred. No.: Score:
                                                  ; TYPE: PRT
; ORGANISM: Homo
US-10-451-168-91
  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. APPLICANT: GLAXO GROUP LIMITED
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
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14 TrpAlaIleTrpValLeuAlaAlaPro-------
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RESULT 5
US-10-433-256-10
; Sequence 10, Application US/10433256
; Publication No. US20040081980A1
; GENERAL INFORMATION:
APPLICANT: SANJANMALA, Madhusudan M.; YAO, Monique G. APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R. APPLICANT: HAFALIA; April J.A.; TANG, Y. Tom APPLICANT: LEE, Ernestine A.; DING, Li
; APPLICANT: HAFALIA; April J.A.; TANG, Y. Tom APPLICANT: LU, Dyung Aina M.; LAL, Preeti G. APPLICANT: WARREN, Bridget A.; YANG, Junning APPLICANT: CHAWLA, Narinder K.; NGUYEN, Danniel B. APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
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; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: LSON, Craig H.
; APPLICANT: LSON, Craig H.
; APPLICANT: LSON, CRAIGH, STANG, JUNGES
; FILE REFERENCE: PI-0313 USN
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/10/433,256
; PRIOR APPLICATION NUMBER: US 60/254,308
; PRIOR APPLICATION NUMBER: US 60/254,308
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte
US-10-433-256-10
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Pred. No.:
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PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL PROGram
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LENGTH: 642
TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-09
PRIOR PRIOR PRIOR DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-03-04
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APPLICANT: SMITHKLINB BEECHAM p.1.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
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CURRENT FILING DATE: 2003-11-12
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APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASHHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT FILING DATE: 2002-03-12
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2375
LENGTH: 525
TYPE: PRT
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Best Local Similarity:
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APPLICANT: SUGITANA
APPLICANT: OTSUKI,
APPLICANT: WAKAMAT
APPLICANT: SATO, H
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                                                          TGGACCAGCACCATCCCC 1650
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg
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YAMAMOTO, JUN-ICHI
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HIO, YURI
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                                       CTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTG
                                                                                                                                                                           CysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSer
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                     GCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACG
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Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: MacDougail, John R.
APPLICANT: Rothenberg, Mark B.
TITLE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR PILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-05
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C Kekuda, Ramesh
Miller, Charles E.
Miller, Charles E.
Miller, Charles B.
Miller, Charles B.
Spytek, Kimberly A.
F. Spytek, Kimberly A.
F. Patturajan, Meera
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Shimkets, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J
Casman, Stacie J.
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
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Edinger, Shlomit R.
Stone, David J.
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Li, Li
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Gusev, Vladimir Y.
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                                                                                                                                                                                                                                       Anderson, David W.
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PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/282,934
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RESULT 9
US-10-381-898-2
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; GENERAL INFORMATION:
; APPLICANT: AZIMZAI, Yalda; BAUGHN,
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Qy 211 CCCCCGCTGGGATTCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270	91 GGCCTTCTGCTGAAGGGCCACAGAGGAACACCCAGGCTGGGATGGAT	Pred. No.: 5.59e-223 Length: 618 Score: 2588.50 Matches: 491 Percent Similarity: 94.62% Conservative: 1 Best Local Similarity: 94.42% Mismatches: 5 Query Match: 81.66% Indels: 23 DB: 15 Gaps: 1 US-10-023-515-3 (1-1746) x US-10-381-898-2 (1-618)	E SEE SEE	; PRIOR FILING DATE: 2000-11-22 ; PRIOR APPLICATION UMBER: US 60/250,567 ; PRIOR FILING DATE: 2000-11-30 ; NUMBER OF SEQ ID NOS: 36 ; SOPTWARE: PERL Program ; SEQ ID NO 2 ; SEQ ID NO 2 ; LENGTH: 618	PRIOR FILING DATE: 2000-10-06 PRIOR PILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: US 60/247,581 PRIOR FILING DATE: 2000-11-09 PRIOR FILING DATE: 2000-11-16 PRIOR FILING DATE: 2000-11-16 PRIOR PILING DATE: 2000-11-16 PRIOR PILING DATE: 2000-11-16 PRIOR PILING DATE: 2000-11-16	FILING DATE: 2001-09-28 PRIOR PELLING DATE: 2003-10-17 PRIOR APPLICATION NUMBER: US/10/381,898 PRIOR APPLICATION NUMBER: PCT/US01/30662 PRIOR FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: US 60/236,947 PRIOR APPLICATION NUMBER: US 60/236,947 PRIOR APPLICATION NUMBER: US 60/238,864	APPLICANT: BOROWSKY, Mark L.; DING, Li; APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.; APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.; APPLICANT: HAPALIA, April J.A.; ISON, Craig H.; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.; APPLICANT: LEE, Ernestine A.; LU, Dyung Aina M.; APPLICANT: RAWKUMAR, Jayalaxmi; RING, Huijun Z.; APPLICANT: RAWKUMAR, Jayalaxmi; RING, Huijun Z.; APPLICANT: SANDANWALA, Madhusudan M.; APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.; APPLICANT: WARREN, Bridget; XU, Yuming; APPLICANT: VANG, Junming; YAO, Monique; YUE, Henry
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\$ \$ \$ \$ \$ \$ \$	B & B &	5	B & B &	Qy Db	& B & B &	5 B 5 B 5	8 8 8 8 8
1291 GATGCTGGTGCACCTGTCTACTACTACTTCGAGCACCGGCCTCACTGCTTTGAAGAC 1350	11/1 GIGGIAALGAARACIACIACAGACAGACAGACAGAGAGAGAGAGAGAGAGAG	GAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGGAGATGTTGCCTGCTGCGCTCAACAAGGACAAGGACAAGATCCTGAGATGCCTCAGTGATATTTGCACCTTTCCCTTTGCCCTCCCATCTGAACAACAACATCCTGGACATCCCGGCCTCAGTATTTTGCACCTTTTGCCACTTTTGCACCTTTTGCACCTTTTGCACCTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTGCACCTTTTTTGCACCTTTTTTGCACCTTTTTTGCACCTTTTTTGCACCTTTTTTGCACCTTTTTTTT	931 CAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGATGGTGCTTTCCTTACTGAGCCTCTA 990		GluseralaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeu TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT	571 ACATGGGATCAGCATGACTCGGGGAACTGGGCCTTCAGGACCAGGTCGATCAGGACCAGGTCGATCAGGACCAGGTCGAGGACCAGGTCGAGGACCAGGTCGAGGACCAGGTCGAGACAGGACCAGGACCAGGACCAGGACCAGGACAGACAAGAACATCGAGACAACATCAAGAACAACATCGAGGACCAGGTGGGGGACCAGCTCTGTGACCATCTTTGGC 690 631 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCAGCTCTGTGACCATCTTTGGC 690	AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC

r—0 m—0 H—0 ⊢	457 GGTGCCTTCAAGACTGGCTCAGCTCCATCTTTGATGGGTCCGCCTGGCTGCTGCTGAGAGACTGGCTCAGCCTCAGCTCCATCTTTGATGGGTCCGCCTGGCTGCTGCTGCTGAGAGACTGGCTCAGACTTGATGAGAGACTGGCTAGAGAACTAGGTAGAGAACTAGATATTAGATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGATATTAGAACTAGAAAAAAAA	Tindels: 15 15 Gaps: 3-515-3 (1-1746) x US-10-104-047-2219 (1-469) 3-515-3 (1-1746) x US-10-104-047-2219 (1-469) 37 ATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAC	; SEQ ID NO 2219 ; LENGTH: 469 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-104-047-2219 Alignment Scores: 5.93e-211 Length: 469 Pred. No.: 2454.00 Matches: 467 Percent Similarity: 100.00% Conservative: 2 Percent Similarity: 99.57% Mismatches: 0	APPLICANT: HELIX RESEARCH INSTITUTE APPLICANT: HELIX RESEARCH INSTITUTE FILE OF INVENTION: No. US20030236392A1el full length cDNA FILE REFERENCE: H1-A0105 CURRENT APPLICATION NUMBER: US/10/104,047 CURRENT FILING DATE: 2002-03-25 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR FILING DATE: NUMBER OF SEQ ID NOS: 4096 SOFTWARE: PATENTIN Ver. 2.1	Qy 1531 GACCTGTCTCTGTGGCCAGCTTATAATCTGACGAGTAGCAGTACCTCCAGCTGGACTTGAAC 1590	1471 AGCCGGAAGATGAAGAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC
Qy 1717 CAGCCTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Qy 1537 TCTCTGTGGCCAGCTTATAATCTGACCAGCTGAACATGAGCATGAACATGAGC 1596	Qy 1357 CCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTTCTTCGTTGTTGTCATGTTGTCTTCCTTC		Qy 1057 GGCTTCCTGCTGCTGAGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTT 1116	Qy 877 GCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCAGAAA 936	Qy 817 AAGAGTGAGGACCTGCAAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAG 876

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CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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                         GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProIleAlaAsnGlyLeu
                                                                            GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCCATGGCCAAAGGCTTA
                                                                                                ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
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                                             TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTG---GAGGCCCAT
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                        Sequence 4, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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TYPE: PRT
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AACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCACCACCATC 1647
                                               AACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTG
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GluGlyValProLeuTrpProAlaTyrThrGlnSerGluGlnTyrLeuLysLeuAspLeu
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                                       PRIOR APPLICATION NUMBER: PCT/USO1/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PEPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR REPLICATION NUMBER: 60/257,048
PRIOR PELLING DATE: 2000-12-20
PRIOR PELLING DATE: 2000-10-09
PRIOR PELLING DATE: 2001-01-09
PRIOR PELLING DATE: 2001-01-09
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PRIOR PELLING DATE: 2001-01-03
PRIOR PELLING DATE: 2001-03-06
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PRIOR PELLING DATE: 2001-03-09
PRIOR PELLING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILLING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR REPLICATION NUMBER: 60/281,535
PRIOR REPLICATION NUMBER: 60/281,535
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US-10-451-168-93
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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                                                                       APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. APPLICANT: GLAXO GROUP LIMITED
   PRIOR
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                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL COMPOUNDS
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: 60/266,797
OR FILING DATE: 2001-02-06
OR APPLICATION NUMBER: 60/276,988
OR FILING DATE: 2001-03-19
OR APPLICATION NUMBER: 60/281,535
OR APPLICATION NUMBER: 60/289,622
OR APPLICATION NUMBER: 60/289,622
OR FILING DATE: 2002-06-28
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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 93
; LENGTH: 356
; TYPE: PAT
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                                      GlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPhe
                                                                                                                      ArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAla
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Sequence 689, Application US/09925298

Publication No. US20020039764A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 689
LENGTH: 549
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Best Local Similarity:
Query Match:
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Pred. No.:
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LOCATION: (1)
OTHER INFORMATION: 3
NAME/KEY: SITE
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ORGANISM: Homo :
FEATURE:
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OTHER INFORMATION:
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                                                                         GlyGlnAspSerAlaSerProlleArgThrThrHisThrGlyGlnValLeuGlySerLeu 35
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SerAlaCysAspGlnValAspSerGluAlaLeuValGlyCysLeuArgGlyLysSerLys 287
TTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTGGGCCGGAAGATGATGAAATACTGGGCT
                                                                                                                              GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMetLysAlaAsp
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|ValMetValTrpIleHisGlyGlyAlaLeuValPheGlyMetAlaSerLeuTyrAspGly
                                                        HisGlyAspGluLeuProPheValPhe---ArgSerPhePheGlyGlyAsnTyrIleLys 465
                                                                               CACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
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CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 689
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Publication No. US20030054421A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapie
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 54
TYPE: PRT
     316 TGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAA 375
                                                                                              271
                                                                                                                                                                  211
                                                                                                                                                                                                                              151 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 HisArgLeuGlnPheTrpLysLysAlaLeuPro 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466
                                                                                                                                                                                                      16 GlyGlnAspSerAlaSerProlleArgThrThrHisThrGlyGlnValLeuGlySerLeu 35
                                                                                                                                                                                                                                                                                                               549
                                                        ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu 95
                                                                                          CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC----
                                                                                                                                ProProLeuGlyProLeuArgPheAlaProProGluProProGluSerTrpSerGlyVal 75
                                                                                                                                                                  CCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cceceerecarrities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnGluGluGlnTyrLeuGlnLeuAsnLeuGlnProAlaValGlyArgAlaLeuLysAla 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAA 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnPheAlaArgAsnGlyAsnProAsnGlyGluGlyLeuProHisTrpProLeuPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAAT 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phe-----ThrGluGluGluGlnLeuSerArgLysMetMetLysTyrTrpAla 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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Matches:
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91
168
24
                                                                                            ----TCAGAG 315
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